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(54) Title: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE PROTEINS

(57) Abstract: The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs, transformed eukaryotic cells expressing these DNAs and antibodies directed to these proteins.

DESCRIPTION

Human Proteins Having Hydrophobic Domains and
DNAs Encoding These Proteins

5

TECHNICAL FIELD

The present invention relates to human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs, eukaryotic cells
10 expressing these DNAs and antibodies directed to these proteins. The proteins of the present invention can be employed as pharmaceuticals or as antigens for preparing antibodies directed to these proteins. The human cDNAs of the present invention can be utilized as probes for genetic
15 diagnosis and gene sources for gene therapy. Furthermore, the cDNAs can be utilized as gene sources for producing the proteins encoded by these cDNAs in large quantities. Cells into which these genes are introduced to express secretory proteins or membrane proteins in large quantities can be
20 utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like. The antibodies of the present invention can be utilized for the detection, quantification, purification and the like of the proteins of the present invention.

25

BACKGROUND ART

Cells secrete many proteins extracellularly. These secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport, the biophylaxis, and the like of the cells. Unlike intracellular proteins, the secretory proteins exert their actions outside the cells. Therefore, they can be administered in the intracorporeal manner such as the injection or the drip, and they possess hidden potentialities as pharmaceuticals. In fact, a number of human secretory proteins such as interferons, interleukins, erythropoietin, thrombolytic agents and the like are currently employed as pharmaceuticals. In addition, secretory proteins other than those described above are undergoing clinical trials for developing their use as pharmaceuticals. It is believed that the human cells produce many unknown secretory proteins. Availability of these secretory proteins as well as genes encoding them is expected to lead to development of novel pharmaceuticals utilizing them.

On the other hand, membrane proteins play important roles, as signal receptors, ion channels, transporters and the like, in the material transport and the signal transduction through the cell membrane. Examples thereof include receptors for various cytokines, ion

channels for the sodium ion, the potassium ion, the chloride ion and the like, transporters for saccharides, amino acids and the like. The genes for many of them have already been cloned. It has been clarified that abnormalities in these
5 membrane proteins are involved in a number of previously cryptogenic diseases. Therefore, discovery of a new membrane protein is expected to lead to elucidation of the causes of many diseases, and isolation of new genes encoding the membrane proteins has been desired.

10 Heretofore, due to difficulty in the purification from human cells, many of these secretory proteins and membrane proteins have been isolated by genetic approaches. A general method is the so-called expression cloning method, in which a cDNA library is introduced into eukaryotic cells
15 to express cDNAs, and the cells secreting, or expressing on the surface of membrane, the protein having the activity of interest are then screened. However, only genes for proteins with known functions can be cloned by using this method.

 In general, a secretory protein or a membrane
20 protein possesses at least one hydrophobic domain within the protein. After synthesis on ribosomes, such domain works as a secretory signal or remains in the phospholipid membrane to be entrapped in the membrane. Accordingly, if the existence of a highly hydrophobic domain is observed in the
25 amino acid sequence of a protein encoded by a cDNA when the

whole base sequence of the full-length cDNA is determined, it is considered that the cDNA encodes a secretory protein or a membrane protein.

5 OBJECTS OF INVENTION

The main object of the present invention is to provide novel human proteins having hydrophobic domains, DNAs coding for these proteins, expression vectors for these DNAs, transformed eucaryotic cells that are capable of
10 expressing these DNAs and antibodies directed to these proteins.

SUMMARY OF INVENTION

As the result of intensive studies, the present
15 inventors have successfully cloned cDNAs encoding proteins having hydrophobic domains from the human full-length cDNA bank, thereby completing the present invention. Thus, the present invention provides a human protein having hydrophobic domain(s), namely a protein comprising any one
20 of amino acid sequences selected from the group consisting of SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130. Moreover, the present invention provides a DNA encoding said protein, exemplified by a cDNA comprising any one of base sequences selected from the group consisting of
25 SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131

to 150, an expression vector that is capable of expressing said DNA by in vitro translation or in eukaryotic cells, a transformed eukaryotic cell that is capable of expressing said DNA and of producing said protein, and an antibody
5 directed to said protein.

This object as well as other objects and advantages of the present invention will become apparent to those skilled in the art from the following description with reference to the accompanying drawings.

10

BRIEF DESCRIPTION OF DRAWINGS

Figure 1: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03613.

15 Figure 2: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03700.

Figure 3: A figure depicting the hydrophobicity/hydrophilicity profile of the protein
20 encoded by clone HP03935.

Figure 4: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10755.

Figure 5: A figure depicting the
25 hydrophobicity/hydrophilicity profile of the protein

encoded by clone HP10760.

Figure 6: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10764.

5 Figure 7: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10768.

Figure 8: A figure depicting the hydrophobicity/hydrophilicity profile of the protein
10 encoded by clone HP10769.

Figure 9: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10784.

Figure 10:A figure depicting the hydrophobicity/hydrophilicity profile of the protein
15 encoded by clone HP10786.

Figure 11:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03727.

20 Figure 12:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03801.

Figure 13:A figure depicting the hydrophobicity/hydrophilicity profile of the protein
25 encoded by clone HP03883.

Figure 14: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03913.

5 Figure 15: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10753.

Figure 16: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10758.

10 Figure 17: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10771.

15 Figure 18: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10778.

Figure 19: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10781.

20 Figure 20: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10785.

Figure 21: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03878.

25 Figure 22: A figure depicting the

hydrophobicity/hydrophilicity profile of the protein
encoded by clone HP03884.

Figure 23:A figure depicting the
hydrophobicity/hydrophilicity profile of the protein
5 encoded by clone HP03934.

Figure 24: A figure depicting the
hydrophobicity/hydrophilicity profile of the protein
encoded by clone HP03949.

Figure 25: A figure depicting the
10 hydrophobicity/hydrophilicity profile of the protein
encoded by clone HP03959.

Figure 26: A figure depicting the
hydrophobicity/hydrophilicity profile of the protein
encoded by clone HP03983.

15 Figure 27: A figure depicting the
hydrophobicity/hydrophilicity profile of the protein
encoded by clone HP10745.

Figure 28: A figure depicting the
hydrophobicity/hydrophilicity profile of the protein
20 encoded by clone HP10775.

Figure 29: A figure depicting the
hydrophobicity/hydrophilicity profile of the protein
encoded by clone HP10782.

Figure 30:A figure depicting the
25 hydrophobicity/hydrophilicity profile of the protein.

Figure 31:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03977.

5 Figure 32:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10649.

Figure 33:A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10779.

10 Figure 34: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10790.

15 Figure 35: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10793.

Figure 36: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10794.

20 Figure 37: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10797.

Figure 38: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10798.

25 Figure 39: A figure depicting the

hydrophobicity/hydrophilicity profile of the protein
encoded by clone HP10800.

Figure 40:A figure depicting the
hydrophobicity/hydrophilicity profile of the protein
5 encoded by clone HP10801.

Figure 41:A figure depicting the
hydrophobicity/hydrophilicity profile of the protein
encoded by clone HP03596.

Figure 42:A figure depicting the
10 hydrophobicity/hydrophilicity profile of the protein
encoded by clone HP03882.

Figure 43:A figure depicting the
hydrophobicity/hydrophilicity profile of the protein
encoded by clone HP03903.

Figure 44: A figure depicting the
15 hydrophobicity/hydrophilicity profile of the protein
encoded by clone HP03974.

Figure 45: A figure depicting the
hydrophobicity/hydrophilicity profile of the protein
20 encoded by clone HP03978.

Figure 46: A figure depicting the
hydrophobicity/hydrophilicity profile of the protein
encoded by clone HP10735.

Figure 47: A figure depicting the
25 hydrophobicity/hydrophilicity profile of the protein

encoded by clone HP10750.

Figure 48: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10777.

5 Figure 49: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10780.

Figure 50: A figure depicting the hydrophobicity/hydrophilicity profile of the protein
10 encoded by clone HP10795.

DETAILED DESCRIPTION OF THE INVENTION

The proteins of the present invention can be obtained, for example, by a method for isolating proteins
15 from human organs, cell lines or the like, a method for preparing peptides by the chemical synthesis based on the amino acid sequence of the present invention, or a method for producing proteins by the recombinant DNA technology using the DNAs encoding the hydrophobic domains of the
20 present invention. Among these, the method for producing proteins by the recombinant DNA technology is preferably employed. For example, the proteins can be expressed in vitro by preparing an RNA by in vitro transcription from a vector having the cDNA of the present invention, and then
25 carrying out in vitro translation using this RNA as a

template. Alternatively, incorporation of the translated region into a suitable expression vector by the method known in the art may lead to expression of the encoded protein in large quantities in prokaryotic cells such as *Escherichia coli* and *Bacillus subtilis*, or eukaryotic cells such as yeasts, insect cells and mammalian cells.

In the case where the protein of the present invention is produced by expressing the DNA by in vitro translation, the protein of the present invention can be produced in vitro by incorporating the translated region of this cDNA into a vector having an RNA polymerase promoter, and then adding the vector to an in vitro translation system such as a rabbit reticulocyte lysate or a wheat germ extract, which contains an RNA polymerase corresponding to the promoter. The RNA polymerase promoters are exemplified by T7, T3, SP6 and the like. The vectors containing promoters for these RNA polymerases are exemplified by pKA1, pCDM8, pT3/T7 18, pT7/3 19, pBluescript II and the like. Furthermore, the protein of the present invention can be expressed in the secreted form or the form incorporated in the microsome membrane when a canine pancreas microsome or the like is added to the reaction system.

In the case where the protein of the present invention is produced by expressing the DNA in a microorganism such as *Escherichia coli*, a recombinant

expression vector in which the translated region of the cDNA of the present invention is incorporated into an expression vector having an origin which is capable of replicating in the microorganism, a promoter, a ribosome-binding site, a cDNA-cloning site, a terminator and the like is constructed. After transformation of the host cells with this expression vector, the resulting transformant is cultured. Thus, the protein encoded by the cDNA can be produced in large quantities in the microorganism. In this case, a protein fragment containing any translated region can be obtained by adding an initiation codon and a termination codon in front of and behind the selected translated region and expressing the protein. Alternatively, the protein can be expressed as a fusion protein with another protein. Only the portion of the protein encoded by the cDNA can be obtained by cleaving this fusion protein with a suitable protease. The expression vectors for *Escherichia coli* are exemplified by the pUC series, pBluescript II, the pET expression system, the pGEX expression system and the like.

In the case where the protein of the present invention is produced by expressing the DNA in eukaryotic cells, the protein of the present invention can be produced as a secretory protein, or as a membrane protein on the surface of cell membrane, by incorporating the translated region of the cDNA into an expression vector for eukaryotic

cells that has a promoter, a splicing region, a poly(A) addition site and the like, and then introducing the vector into the eukaryotic cells. The expression vectors are exemplified by pKA1, pED6dpc2, pCDM8, pSVK3, pMSG, pSVL, 5 pBK-CMV, pBK-RSV, EBV vectors, pRS, pYES2 and the like. Examples of eukaryotic cells to be used in general include mammalian cultured cells such as monkey kidney COS7 cells and Chinese hamster ovary CHO cells, budding yeasts, fission yeasts, silkworm cells, and Xenopus oocytes. Any eukaryotic 10 cells may be used as long as they are capable of expressing the proteins of the present invention. The expression vector can be introduced into the eukaryotic cells by using a method known in the art such as the electroporation method, the calcium phosphate method, the liposome method and the 15 DEAE-dextran method.

After the protein of the present invention is expressed in prokaryotic cells or eukaryotic cells, the protein of interest can be isolated and purified from the culture by a combination of separation procedures known in 20 the art. Examples of the separation procedures include treatment with a denaturing agent such as urea or a detergent, sonication, enzymatic digestion, salting-out or solvent precipitation, dialysis, centrifugation, ultrafiltration, gel filtration, SDS-PAGE, isoelectric 25 focusing, ion-exchange chromatography, hydrophobic

chromatography, affinity chromatography and reverse phase chromatography.

The proteins of the present invention also include peptide fragments (of 5 amino acid residues or more) containing any partial amino acid sequences in the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130. These peptide fragments can be utilized as antigens for preparation of antibodies. Among the proteins of the present invention, those having the signal sequences are secreted in the form of mature proteins after the signal sequences are removed. Therefore, these mature proteins shall come within the scope of the protein of the present invention. The N-terminal amino acid sequences of the mature proteins can be easily determined by using the method for the determination of cleavage site of a signal sequence [JP-A 8-187100]. Furthermore, some membrane proteins undergo the processing on the cell surface to be converted to the secreted forms. Such proteins or peptides in the secreted forms shall also come within the scope of the protein of the present invention. In the case where sugar chain-binding sites are present in the amino acid sequences of the proteins, expression of the proteins in appropriate eukaryotic cells affords the proteins to which sugar chains are added. Accordingly, such proteins or peptides to which sugar chains are added shall also come

within the scope of the protein of the present invention.

The DNAs of the present invention include all the DNAs encoding the above-mentioned proteins. These DNAs can be obtained by using a method for chemical synthesis, a
5 method for cDNA cloning and the like.

The cDNAs of the present invention can be cloned, for example, from cDNA libraries derived from the human cells. The cDNAs are synthesized by using poly(A)⁺ RNAs extracted from human cells as templates. The human cells may
10 be cells delivered from the human body, for example, by the operation or may be the cultured cells. The cDNAs can be synthesized by using any method such as the Okayama-Berg method [Okayama, H. and Berg, P., Mol. Cell. Biol. 2: 161-170 (1982)], the Gubler-Hoffman method [Gubler, U. and
15 Hoffman, J., Gene 25: 263-269 (1983)] and the like. However, it is desirable to use the capping method [Kato, S. et al., Gene 150: 243-250 (1994)], as exemplified in Examples, in order to obtain a full-length clone in an effective manner. In addition, commercially available human cDNA libraries can
20 be utilized. The cDNAs of the present invention can be cloned from the cDNA libraries by synthesizing an oligonucleotide on the basis of base sequences of any portion in the cDNA of the present invention and screening the cDNA libraries using this oligonucleotide as a probe for
25 colony or plaque hybridization according to a method known

in the art. In addition, the cDNA fragments of the present invention can be prepared from an mRNA isolated from human cells by the RT-PCR method in which oligonucleotides which hybridize with both termini of the cDNA fragment of interest
5 are synthesized, which are then used as the primers.

The cDNAs of the present invention are characterized in that they comprise any one of the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110 and 131 to 140 or the base sequences
10 represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141 to 150. Table 1 summarizes the clone number (HP number), the cells from which the cDNA clone was obtained, the total number of bases of the cDNA, and the number of the amino acid residues of the encoded protein,
15 for each of the cDNAs.

Table 1

Sequence No.	HP No.	Cell	Number of bases	Number of amino acids
1, 11, 21	HP03613	Kidney	2865	578
2, 12, 22	HP03700	Kidney	3323	243
3, 13, 23	HP03935	Kidney	1585	461
4, 14, 24	HP10755	Kidney	2122	647
5, 15, 25	HP10760	Kidney	1775	446
6, 16, 26	HP10764	Kidney	1372	197
7, 17, 27	HP10768	Kidney	2074	540
8, 18, 28	HP10769	Kidney	2252	442
9, 19, 29	HP10784	Kidney	1461	262
10, 20, 30	HP10786	Kidney	1122	152
31, 41, 51	HP03727	Kidney	1617	335
32, 42, 52	HP03801	Umbilical cord blood	1749	208
33, 43, 53	HP03883	Kidney	1402	406
34, 44, 54	HP03913	Kidney	2474	618
35, 45, 55	HP10753	Umbilical cord blood	3296	208
36, 46, 56	HP10758	Kidney	1818	502
37, 47, 57	HP10771	Kidney	1646	336
38, 48, 58	HP10778	Kidney	1416	340
39, 49, 59	HP10781	Kidney	1927	223
40, 50, 60	HP10785	Kidney	1419	309
61, 71, 81	HP03878	Kidney	2016	599
62, 72, 82	HP03884	Kidney	1446	81
63, 73, 83	HP03934	Kidney	2467	654
64, 74, 84	HP03949	Kidney	1450	390
65, 75, 85	HP03959	Kidney	1897	452

Table 1 (continued)

Sequence No.	HP No.	Cell	Number of bases	Number of amino acids
66, 76, 86	HP03983	Kidney	1856	490
67, 77, 87	HP10745	Umbilical cord blood	2173	392
68, 78, 88	HP10775	Kidney	1934	538
69, 79, 89	HP10782	Kidney	1880	102
70, 80, 90	HP10787	Kidney	2295	442
91, 101, 111	HP03977	Kidney	1894	227
92, 102, 112	HP10649	KB	2413	352
93, 103, 113	HP10779	Kidney	2376	130
94, 104, 114	HP10790	Kidney	1155	330
95, 105, 115	HP10793	Kidney	1329	350
96, 106, 116	HP10794	Kidney	1387	113
97, 107, 117	HP10797	Kidney	1158	189
98, 108, 118	HP10798	Kidney	1106	277
99, 109, 119	HP10800	Kidney	1907	274
100, 110, 120	HP10801	Kidney	1816	390
121, 131, 141	HP03696	Umbilical cord blood	1961	395
122, 132, 142	HP03882	Kidney	2194	550
123, 133, 143	HP03903	Kidney	2753	218
124, 134, 144	HP03974	Kidney	2085	596
125, 135, 145	HP03978	Kidney	2208	467
126, 136, 146	HP10735	Umbilical cord blood	2044	476
127, 137, 147	HP10750	Umbilical cord blood	2176	449
128, 138, 148	HP10777	Kidney	1363	105
129, 139, 149	HP10780	Kidney	1043	81
130, 140, 150	HP10795	Kidney	2435	552

The same clones as the cDNAs of the present

invention can be easily obtained by screening the cDNA libraries constructed from the human cell lines or human tissues utilized in the present invention using an oligonucleotide probe synthesized on the basis of the base sequence of the cDNA provided in any one of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131 to 150.

In general, the polymorphism due to the individual differences is frequently observed in human genes. Accordingly, any cDNA in which one or plural nucleotides are added, deleted and/or substituted with other nucleotides in SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131 to 150 shall come within the scope of the present invention.

Similarly, any protein in which one or plural amino acids are added, deleted and/or substituted with other amino acids resulting from the above-mentioned changes shall come within the scope of the present invention, as long as the protein possesses the activity of the protein having any one of the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130.

The cDNAs of the present invention also include cDNA fragments (of 10 bp or more) containing any partial base sequence in the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110 and 131 to 140 or in the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141 to 150. Also, DNA

fragments each consisting of a sense strand and an anti-sense strand shall come within this scope. These DNA fragments can be utilized as the probes for the genetic diagnosis.

5 The antibody of the present invention can be obtained from a serum after immunizing an animal using the protein of the present invention as an antigen. A peptide that is chemically synthesized based on the amino acid sequence of the present invention and a protein expressed in
10 eukaryotic or prokaryotic cells can be used as an antigen. Alternatively, an antibody can be prepared by introducing the above-mentioned expression vector for eukaryotic cells into the muscle or the skin of an animal by injection or by using a gene gun and then collecting a serum therefrom [JP-A
15 7-313187]. Animals that can be used include a mouse, a rat, a rabbit, a goat, a chicken and the like. A monoclonal antibody directed to the protein of the present invention can be produced by fusing B cells collected from the spleen of the immunized animal with myelomas to generate hybridomas.

20 In addition to the activities and uses described above, the polynucleotides and proteins of the present invention may exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for
25 proteins of the present invention may be provided by

administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

5 Research Uses and Utilities

 The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or
10 therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome
15 markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive
20 PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise
25 anti-protein antibodies using DNA immunization techniques;

and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction),
5 the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

10 The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled
15 reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or
20 development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding
25 occurs or to identify inhibitors of the binding interaction.

Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable
5 of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation
10 "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

15 Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source,
20 use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or
25 capsules. In the case of microorganisms, the protein or

polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

5 A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to
10 date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present
15 invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

 The activity of a protein of the invention may,
20 among other means, be measured by the following methods:

 Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene
25 Publishing Associates and Wiley-Interscience (Chapter 3, In

Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 5 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or 10 thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , 15 Schreiber, R.D. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without 20 limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205- 25 1211, 1991; Moreau et al., Nature 336:690-692, 1988;

Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6-
Nordan, R. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons,
5 Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 -
Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1
pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement
10 of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In Current Protocols in
Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens
15 (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by
measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in
Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing
20 Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines
and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA
25 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun.

11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a

protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable

from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding

costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and

thereby activate, T cells in vivo.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II

molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan,

A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al.,
5 Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-
10 2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341,
15 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without
20 limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J.J. and Brunswick, M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

25 Mixed lymphocyte reaction (MLR) assays (which will

identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which

will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 5 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 10 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 15 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the 20 treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells 25 alone or in combination with other cytokines, thereby

indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complementary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited
5 above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular
10 Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate
15 lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA
20 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology
25 22:353-359, 1994; Cobblestone area forming cell assay,

Ploemacher, R.E. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

10 Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial

defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to
5 attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by
10 blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present
15 invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or
20 ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and
25 in repairing defects to tendon or ligament tissue. De novo

tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in
5 cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or
10 ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The
15 compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the
20 treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral
25 nervous system, such as peripheral nerve injuries,

peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A

protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include,

without limitation, those described in: Vale et al.,
Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-
782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et
al., Nature 318:659-663, 1985; Forage et al., Proc. Natl.
5 Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have
chemotactic or chemokinetic activity (e.g., act as a
chemokine) for mammalian cells, including, for example,
10 monocytes, fibroblasts, neutrophils, T-cells, mast cells,
eosinophils, epithelial and/or endothelial cells.
Chemotactic and chemokinetic proteins can be used to
mobilize or attract a desired cell population to a desired
site of action. Chemotactic or chemokinetic proteins provide
15 particular advantages in treatment of wounds and other
trauma to tissues, as well as in treatment of localized
infections. For example, attraction of lymphocytes,
monocytes or neutrophils to tumors or sites of infection may
result in improved immune responses against the tumor or
20 infecting agent.

A protein or peptide has chemotactic activity for
a particular cell population if it can stimulate, directly
or indirectly, the directed orientation or movement of such
cell population. Preferably, the protein or peptide has the
25 ability to directly stimulate directed movement of cells.

Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

5 The activity of a protein of the invention may, among other means, be measured by the following methods:

 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce
10 the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E.
15 Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995;
20 Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

 A protein of the invention may also exhibit
25 hemostatic or thrombolytic activity. As a result, such a

protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke)).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and

their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein

of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or cardiac cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization,

storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Examples

The present invention is specifically illustrated in more detail by the following Examples, but Examples are not intended to restrict the present invention. The basic procedures with regard to the recombinant DNA and the enzymatic reactions were carried out according to the

literature ["Molecular Cloning. A Laboratory Manual", Cold Spring Harbor Laboratory, 1989]. Unless otherwise stated, restriction enzymes and various modifying enzymes to be used were those available from Takara Shuzo. The buffer compositions and the reaction conditions for each of the enzyme reactions were as described in the attached instructions. The cDNA synthesis was carried out according to the literature [Kato, S. et al., Gene 150: 243-250 (1994)].

10 (1) Selection of cDNAs Encoding Proteins Having Hydrophobic Domains

 The cDNA library of epidermoid carcinoma cell line KB (W098/11217), and the cDNA libraries constructed from human kidney mRNA (Clontech) and human umbilical cord blood mRNA were used as cDNA libraries.

 Full-length cDNA clones were selected from the respective libraries and the whole base sequences thereof were determined to construct a homo-protein cDNA bank consisting of the full-length cDNA clones. The hydrophobicity/hydrophilicity profiles were determined for the proteins encoded by the full-length cDNA clones registered in the homo-protein cDNA bank by the Kyte-Doolittle method [Kyte, J. & Doolittle, R. F., J. Mol. Biol. 157: 105-132 (1982)] to examine the presence or absence of a hydrophobic domain. A clone that has a hydrophobic region

being assumed as a secretory signal or a transmembrane domain in the amino acid sequence of the encoded protein was selected as a clone candidate.

(2) Protein Synthesis by In Vitro Translation

5 The plasmid vector bearing the cDNA of the present invention was used for in vitro transcription/translation with a T_NT rabbit reticulocyte lysate kit (Promega). In this case, [³⁵S]methionine was added to label the expression product with a radioisotope. Each of the reactions was
10 carried out according to the protocols attached to the kit. Two micrograms of the plasmid was subjected to the reaction at 30°C for 90 minutes in the reaction solution of a total volume of 25 µl containing 12.5 µl µ of T_NT rabbit reticulocyte lysate, 0.5 µl of a buffer solution (attached
15 to the kit), 2 µl of an amino acid mixture (without methionine), 2 µl of [³⁵S]methionine (Amersham) (0.37 MBq/µl), 0.5 µl of T7 RNA polymerase, and 20 U of RNasin. The experiment in the presence of a membrane system was carried out by adding 2.5 µl of a canine pancreas microsome fraction
20 (Promega) to the reaction system. 2 µl of the SDS sampling buffer (125 mM Tris-hydrochloride buffer, pH 6.8, 120 mM 2-mercaptoethanol, 2% SDS solution, 0.025% Bromophenol Blue and 20% glycerol) was added to 3 µl of the reaction solution. The resulting mixture was heated at 95°C for 3 minutes and
25 then subjected to SDS-polyacrylamide gel electrophoresis.

The molecular weight of the translation product was determined by carrying out the autoradiography.

(3) Expression in COS7

Escherichia coli cells harboring the expression
5 vector for the protein of the present invention were
cultured at 37°C for 2 hours in 2 ml of the 2 x YT culture
medium containing 100 µg/ml of ampicillin, the helper phage
M13KO7 (50 µl) was added thereto, and the cells were then
cultured at 37°C overnight. Single-stranded phage particles
10 were obtained by polyethylene glycol precipitation from a
supernatant separated by centrifugation. The particles were
suspended in 100 µl of 1 mM Tris-0.1 mM EDTA, pH 8 (TE).

The cultured cells derived from monkey kidney,
COS7, were cultured at 37°C in the presence of 5% CO₂ in the
15 Dulbecco's modified Eagle's medium (DMEM) containing 10%
fetal calf serum. 1 x 10⁵ COS7 cells were inoculated into a
6-well plate (Nunc, well diameter: 3 cm) and cultured at
37°C for 22 hours in the presence of 5% CO₂. After the medium
was removed, the cell surface was washed with a phosphate
20 buffer solution followed by DMEM containing 50 mM Tris-
hydrochloride (pH 7.5) (TDMEM). A suspension containing 1 µl
of the single-stranded phage suspension, 0.6 ml of the DMEM
medium and 3 µl of TRANSFECTAMTM (IBF) was added to the cells
and the cells were cultured at 37°C for 3 hours in the
25 presence of 5% CO₂. After the sample solution was removed,

the cell surface was washed with TDMEM, 2 ml per well of DMEM containing 10% fetal calf serum was added, and the cells were cultured at 37°C for 2 days in the presence of 5% CO₂. After the medium was exchanged for a medium containing
5 [35S]cysteine or [35S]methionine, the cells were cultured for one hour. After the medium and the cells were separated each other by centrifugation, proteins in the medium fraction and the cell membrane fraction were subjected to SDS-PAGE.

(4) Preparation of Antibodies

10 A plasmid vector containing the cDNA of the present invention was dissolved in a phosphate buffer solution (PBS: 145 mM NaCl, 2.68 mM KCl, 8.09 mM Na₂HPO₄, 2 mM KH₂PO₄, pH 7.2) at a concentration of 2 µg/µl. 25 µl each (a total of 50 µl) of the thus prepared plasmid solution in
15 PBS was injected into the right and left musculi quadriceps femoris of three mice (ICR line) using a 26 guage needle. After similar injections were repeated for one month at intervals of one week, blood was collected. The collected blood was stored at 4°C overnight to coagulate the blood,
20 and then centrifuged at 8,000 x g for five minutes to obtain a supernatant. NaN₃ was added to the supernatant to a concentration of 0.01% and the mixture was then stored at 4°C. The generation of an antibody was confirmed by immunostaining of COS7 cells into which the corresponding
25 vector had been introduced, or by Western blotting using a

cell lysate or a secreted product.

(5) Clone Examples

<HP03613> (SEQ ID NOS: 1, 11, and 21)

Determination of the whole base sequence of the
5 cDNA insert of clone HP03613 obtained from cDNA library of
human kidney revealed the structure consisting of a 337-bp
5'-untranslated region, a 1737-bp ORF, and a 791-bp 3'-
untranslated region. The ORF encodes a protein consisting of
578 amino acid residues and there existed eleven putative
10 transmembrane domains. Figure 1 depicts the
hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
of high molecular weight.

15 The search of the protein database using the amino
acid sequence of the present protein revealed that the
protein was similar to mouse organic cation transporter-
like protein (Accession No. BAA23875). Table 2 shows the
comparison between amino acid sequences of the human protein
20 of the present invention (HP) and mouse organic cation
transporter-like protein (MT). Therein, the marks of -, *,
and . represent a gap, an amino acid residue identical with
that of the protein of the present invention, and an amino
acid residue similar to that of the protein of the present
25 invention, respectively. The both proteins shared a homology

of 70.4% in the entire region.

Table 2

```

5  HP MAFSELDDLVGGLGRFQVLQTMALMVSIMWLCTQSMLNFSAAVPSHRCWAPLLDNSTAQ
    ***.**** *****. **. **. . *. *. **. ***** *****. *****. *
    MT MAFPELLDRVGGLGRFQLFQTVALVTPILWVTTQNMLENFSAAVPHRCWVPLLDNSTSQ

    HP ASILGSLSPEALLAISIPPGPNQRPHQCRRFRQPQWQLDPNATATSWSEADTEPCVDGW
10  *** *. *. *. .***. *****. *. ***** .. *****. **. *. **** ***
    MT ASIPGDLGPDVLLAVSIPPGPDQQPHQCLRFRQPQWQLTESNATATNWSDAATEPCEDGW

    HP VYDRSIFTSTIVAKWNLVCDSHALKPMAQSIYLAGILVGAAACGPASDRFGRRLVLTWSY
    ***. *. * ****. . *. ***. *. **. *****. *****. **. ***** *****
15  MT VYDHSTFRSTIVTTWDLVCNSQALRPMAQSIFLAGILVGAAVCGHASDRFGRRRVLTWSY

    HP LQMAVMGTAAAFAPAFPVYCLFRFLLAFVAVAGVMMNTGTLRRSLTWRHAGGLHAGSRAEP
    * . . * ***** *. **. ***** *****..
    MT LLVSVSGTAAAFMPTFPLYCLFRFLLASAVAGVMMNTAS-----

20  HP LGLLAVMEWTAARARPLVMTLNSLGFSGHGLTAAVAYGVRDWTLQLVVSVPFFLCFLY
    . ****. *. . . *****. *****. **. . *****. * . ***. **. **** *. *
    MT ----LLMEWTSAGGSPLVMTLNLGFSFGQVLTGSVAYGVRSWRMLQLAVSAPFFLFFVY

25  HP SWWLAESARWLLTTGRLDWGLQELWRVAAINGKAVQDTLTPEVLLSAMREELSMGQPPA

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****.*****.*.*.* ***** *****.*.* ***** **** ** *... *
MT SWWLPESARWLITVGKLDQGLQELQRVAAVNRRKAEGDTLTMEVLRSAMEEEPSRDKAGA

HP SLGTLLRMPGLRFRTCISTLCWFAGFTFFGLALDLQALGSNIFLLQMFIGVVDIPAKMG
5 *****. ***** ** ** *****.*****.*****.***.***.*.*
MT SLGTLLHTPGLRHRTIISMLCWFAGFTFYGLALDLQALGSNIFLLQALIGIVDFPVKTG

HP ALLLSHLGRRPTLAASLLLAGLCILANTLVPHEMGALRSALAVLGLGGVGAAFTCITIY
...*.***. ....*.*.*****.*.*****.***.*****.*****.
10 MT SLLISRLGRRLCQVSFLVLPGLCILSNILVPHGMGVLRSALAVLGLGCLGGAFTCITIF

HP SSELFPTVLRMTAVGLGQMAARGGAILGPLVRLLGVHGPWLPLLVGTVPVLSGLAALLL
*****.*****.*.*****.*****.*.*.*****.*****.
MT SSELFPTVIRMTAVGLCQVAARGGAMLGPLVRLLGVYGSWMPLLVGVPVLSGLAALLL
15

HP PETQSLPLPDTIQDVQNAVKKATHGTLGNSVLKSTQF
***.*****.*.*.***.*.*..*.*.*..
MT PETKNLPLPDTIQDIKQSVKKVTHDTPDGSILMSTRL

```

20 The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of
sequences that shared a homology of 90% or more (for example,
Accession No. AI792236). However, since they are partial
sequences, it can not be judged whether or not they encode
25 the same protein as the protein of the present invention.

<HP03700> (SEQ ID NOS: 2, 12, and 22)

Determination of the whole base sequence of the cDNA insert of clone HP03700 obtained from cDNA library of human kidney revealed the structure consisting of a 45-bp 5'-untranslated region, a 732-bp ORF, and a 2546-bp 3'-untranslated region. The ORF encodes a protein consisting of 243 amino acid residues and there existed three putative transmembrane domains. Figure 2 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was somewhat larger than the molecular weight of 25,561 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse yolk sac permease-like molecule 1 (Accession No. AAA92292). Table 3 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse yolk sac permease-like molecule 1 (MY). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 74.5% in the N-terminal region of 231 amino acid residues.

Table 3

HP MSRSPLNPSQLRSVGSQDALAPLPP--PAPQNPSTHSWDP-LCGSLPWGLSCLLALQHVL
 5 *****.*.*.*.*.*****.*.*****.***. .*.*****.*
 MY MSRSPLHPIPLLSEGYQDTPAPLPPLPPLQNPSSRSWASRVFGPSTWGLSCLLALQHFL

 HP VMASLLCVSHLLLLCSLSPGGLSYSPSQLASSFFSCGMSTILQTMGSRLPLVQAPSLE
 *.***.*****.*.*****.*.*****.***.*****.*****
 10 MY VLASLLWASHLLLLHGLPPGGLSYPPAQLASSFFSCGLSTVLQTMGSRLPLIQAPSLE

 HP FLIPALVLTSQLPRAIQTPGNSSLMLHLCR-GPSCHGLGHWNTSLQEVS GAVVVSGLLQ
 *****.***. .*.***.***.*.***. .*.***.*****.*****
 MY FLIPALVLTNQLPLTTKTPGNASLSLPLCSLTRSCHGLELWNTSLREVSGAVVVSGLLQ
 15
 HP GMMGLLGSPGHVFP HCGPLVLAPSLV VAGLSAHREVAQFCFTHWGLALLYVSPERRGMVP
 *.***.***.*****.*****.*****.*****.
 MY GTIGLLGVPGRVFPYCGPLVLAPSLV VAGLSAHKEVAQFCSAHWGLALLLILLMVVCSQH

 20 HP SGGVWGD

 MY LGSCQIPLCSWRPSSTSTHICIPVFRLLSVLAPVACVWFISAFVGTSVIPLQLSEPSDAP

The search of the GenBank using the base sequences
 25 of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example, Accession No. AW167520). However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5 <HP03935> (SEQ ID NOS: 3, 13, and 23)

Determination of the whole base sequence of the cDNA insert of clone HP03935 obtained from cDNA library of human kidney revealed the structure consisting of a 72-bp 5'-untranslated region, a 1386-bp ORF, and a 127-bp 3'-untranslated region. The ORF encodes a protein consisting of 461 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 3 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 56 kDa that was somewhat larger than the molecular weight of 52,052 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 61 kDa. In addition, there exists in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Ser-Ser at position 193 and Asn-Ser-Thr at position 236). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from histidine at position 32.

10
15
20
25

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Arabidopsis thaliana* hypothetical protein (Accession No. CAB41318). Table 4 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Arabidopsis thaliana* hypothetical protein (AT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 30.8% in the intermediate region of 214 amino acid residues.

Table 4

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HP MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPEKSSTKETERKETKAE
HP ELDAEVLEVFPHEWQALQPGQAVPAGSHVRLNLQTGEREAKLOYEDKFRNNLKGKRLD
AT  MPTIFFFRYVFLLVVISLVGFSIAEKNSSGGMVWSSVRDEAELVEDSGVVIGEQQD
HP INTNTYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIET
      *.....*.....*...***. ...*...
AT IDGGFSSLDGMLHWAIGHSDPATLKEAAKDAEKMS-LDELQKRQLELKEKVEKLG--MPS

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AT NAKLMQIAIDDLNSSLSEDRHRALQELLILVEPIDNANDLSKSGGLRVVAGELNHDDT

HP LVKEYAAFVLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHF

AT EVRKLAAWVLGKASQNNPFVQEQVLELGALTT-LIKMVNSSSTEEAVKALFAVSALIRNN

HP PYAQRQFLKLGGQLVRLTLVQEKGTEV-LAVRVVTLLYDLVTEKMFEEEEAELTQEMSPE

AT IAGQDLFFAAHGYIMLRDVMNNGSLDMKLRRKAVFLVGDLAESQLQNTKDELPIFKDRL

HP KLQQYRQVHLLPGLWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLG

AT FLKSVVDLIVVLDLQEKALTAIQTLQLKSI EPQVLKESCGLEEALERMKLQLEESMA

HP RTLASLQA EYQVLASLELQDGEDEGYFQELLGSVNSLLKELR

AT DEYKRDYAADVESIRGEVELIFRQKLGLL

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW025017) among ESTs. However, since they are

partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10755> (SEQ ID NOS: 4, 14, and 24)

5 Determination of the whole base sequence of the cDNA insert of clone HP10755 obtained from cDNA library of human kidney revealed the structure consisting of a 55-bp 5'-untranslated region, a 1944-bp ORF, and a 123-bp 3'-untranslated region. The ORF encodes a protein consisting of
10 647 amino acid residues and there existed eight putative transmembrane domains. Figure 4 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product
15 of high molecular weight.

 The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human hypothetical protein KIAA0062 (Accession No. BAA06685). Table 5 shows the comparison
20 between amino acid sequences of the human protein of the present invention (HP) and human hypothetical protein KIAA0062 (KI). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue
25 similar to that of the protein of the present invention,

respectively. The both proteins shared a homology of 30.6% in the C-terminal region of 408 amino acid residues.

Table 5

5	HP MASLVSLELGLLLAVLVVTATASPPAGLLSLLTSGQGALDQEALGGLLNTLADRVHCTNG
	HP PCGKCLSVEDALGLGEPEGSGLP GPVLEARYVARLSAAAVLYLSNPEGTCEDTRAGLWA
10	HP SHADHLLALLESPKALTPGLSWLLQRMQARAAGQTPKTACVDIPQLLEEAVGAGAPGSAG
	KI RVIADAPAKLLPPPAWDLAVRLRGAEAAASERQVYSVTM
	HP GVLAALLDHVRSGSCFHALPSPQYFVDFVFQHSSEVPMTLAELSALMQRLGVGREAHSD
15	KI KLLLLHPAFQSCLLLTLLGLWRTTPEAHASSLGAPAIASAASFLQDLIHRYGEGDSLTLQQ
	HP HSHRHRGASSRDPVPLISSNSSSVWDTVCLSARDVMAAYGLSEQAGVTPEAWAQLSPAL
	..*. *. *...*...***.*..
20	KI LKALLNHLDVGVGRGNVTQHVGQHRNLSTCFSSGDLFTAHNFSEQSRIGSSELQEFCTI
	HP LQQQLSGACTSQSRPPVQDQLSQSER-----YLYGSLATLLICLCAVFGLLLLTCTGCR
	*** * ****... ..*...*...*...*...*
25	KI LQQLDSTRACTSENQENEENEQTEGRPSAVEVWGYGLLCVTVISLCSLLGASVVPFMK-K

HP GVAHYILQTFSLAVGALTGDAVLHLTPKVLGLHTHSEGLSPQPTWRLLAMLAGLYAFF
 . . . * *..**.* * ..*...*.*...*... **.* **
 KI TFYKRLLLYFIALAIGTLYSNALFQLIPEAFGFNPL-EDYYVSKSA----VVFGGFYLFF

 5 HP LFENLFNLLL-PRDPEDLEDGPCGHSS-HSHGGHSHGVSLLAPSELRQPKPPH----EG
 . *.** * . * ** . * . . . * . * .
 KI FTEKILKILLKQKNEHHHGHSHYASESLPSKKDQEEGVMEKLQNGDLDMIPQHCSSELD

 HP SRADLVAE-----ESPELLNPE-----PRRLS-PELRLLPYMITLGDAVHNFADGLAV
 10 . . * . * . * . . . * * . . ****. * . . *** ****.
 KI GKAPMVDEKVIVGSLSVQDLQASQSACYWLKGVRYSDIGTLAWMITLSDGLHNFIDGLAI

 HP GAAFASSWKTGLATSLAVFCHPELPHLGDFALLHAGLSVRQALLNLASALTAFAGLYV
 .*. * * . *...*.*.*.*****. **.*.*.***.*. * . **
 15 KI GASFTVSVFQGISTSVAILCEEFPHELGDVFILLNAGMSIQQALFFNFLSACCCYLGLAF

 HP ALAVGVSEESEAWILAVATGLFLYVALCDMLPAMLKV-----RDPRPWLLFLLHNVGLLG
 . . . * * . *..**.*.*.*.***.* * . * . * . * . * . * . * . * . * . * . * .
 KI GILAG-SHFSANWIFALAGGMFLYISLADMFPENNEVCQEDERKGSILIPFIIQNLGLLT
 . 20
 HP GWTVLLLLSLYEDDITF
*.*...*
 KI GFTIMVVLTMYSGQIQIG

 25

Furthermore, the search of the GenBank using the

base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA42490) among ESTs. However, since they are partial sequences, it can not be
5 judged whether or not they encode the same protein as the protein of the present invention.

<HP10760> (SEQ ID NOS: 5, 15, and 25)

Determination of the whole base sequence of the cDNA insert of clone HP10760 obtained from cDNA library of
10 human kidney revealed the structure consisting of a 61-bp 5'-untranslated region, a 1341-bp ORF, and a 373-bp 3'-untranslated region. The ORF encodes a protein consisting of 446 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 5 depicts the
15 hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 48 kDa that was somewhat smaller than the molecular weight of 49,468 predicted from the ORF. In this case, the
20 addition of a microsome led to the formation of a product of 50 kDa. In addition, there exists in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Ala-Thr at position 144 and Asn-Ile-Ser at position 243). Application of the (-3,-1) rule, a method for
25 predicting the cleavage site of the secretory signal

sequence, allows to expect that the mature protein starts from glutamic acid at position 27.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human 25 kDa trypsin inhibitor (Accession No. BAA25066). Table 6 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human 25 kDa trypsin inhibitor (TI). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 33.5% in the intermediate region of 185 amino acid residues.

Table 6

HP MLHPETSPGRGHLLAVLLALLGTAWAEVWPPQLQEAPMAG

20 TI MIAISAVSSALLFSLCEASTVLLNSTDSSPTNNFTDIEAALKAQLDSADIPKARRKR

HP ALNRKESFLLLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLW

..... . *. **..*. * ****.* . *...**. *.** ** * * * *

TI YISQNDMIAILDYHNQVRGKVFPPAANMEYMWVDENLAKSAEAWAATC-IWDHG-PSYLL

```

HP  RTLQVGWNMQLLPAGLASFVEVSLWFAEGQRYSHA-AGEC-----AR--NATCTHYTQL
      * * . . . . . *....* *...* * . . . . *      * .. *****.
TI  RFLGQN--LSVRTGRYRSILQLVKPWYDEVKDYAFPYPQDCNPRCPMRCFGPMCTHYTQM

5   HP  VWATSSQLGCGRHLCSAGQA--AI---EAF-VCAYSPGGNWEVNGKTIIPYKKGAWCSLC
      *****...**.* * . . . . . . . . . . **.*.* *** *.. *** *. ** *
TI  VWATSNRIGCAIHTCQNMNVWGSVWRRAYLVLCNYAPKGNW--IGEA--PYKVGVPCCSSC

HP  TASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCHCHCPPGYTGRYCQVRCSLQ
10  ..*.*
TI  PPSYGGGCTDNLCPGVTSNLYWFK

```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792411) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

20 <HP10764> (SEQ ID NOS: 6, 16, and 26)

Determination of the whole base sequence of the cDNA insert of clone HP10764 obtained from cDNA library of human kidney revealed the structure consisting of a 326-bp 5'-untranslated region, a 594-bp ORF, and a 452-bp 3'-untranslated region. The ORF encodes a protein consisting of

25

197 amino acid residues and there existed two putative transmembrane domains. Figure 6 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro
5 translation resulted in formation of a translation product of 25 kDa that was somewhat larger than the molecular weight of 21,508 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of
10 sequences that shared a homology of 90% or more (for example, Accession No. H45965) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

15 <HP10768> (SEQ ID NOS: 7, 17, and 27)

Determination of the whole base sequence of the cDNA insert of clone HP10768 obtained from cDNA library of human kidney revealed the structure consisting of a 100-bp 5'-untranslated region, a 1623-bp ORF, and a 351-bp 3'-
20 untranslated region. The ORF encodes a protein consisting of 540 amino acid residues and there existed nine putative transmembrane domains. Figure 7 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro
25 translation resulted in formation of a translation product

of high molecular weight.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA459236) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10769> (SEQ ID NOS: 8, 18, and 28)

Determination of the whole base sequence of the cDNA insert of clone HP10769 obtained from cDNA library of human kidney revealed the structure consisting of a 11-bp 5'-untranslated region, a 1329-bp ORF, and a 912-bp 3'-untranslated region. The ORF encodes a protein consisting of 442 amino acid residues and there existed two putative transmembrane domains. Figure 8 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 52 kDa that was somewhat larger than the molecular weight of 49,101 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI625881) among ESTs. However, since they are

partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10784> (SEQ ID NOS: 9, 19, and 29)

5 Determination of the whole base sequence of the
cDNA insert of clone HP10784 obtained from cDNA library of
human kidney revealed the structure consisting of a 60-bp
5'-untranslated region, a 789-bp ORF, and a 612-bp 3'-
untranslated region. The ORF encodes a protein consisting of
10 262 amino acid residues and there existed six putative
transmembrane domains. Figure 9 depicts the
hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
15 of 28 kDa that was almost identical with the molecular
weight of 27,551 predicted from the ORF.

The search of the protein database using the amino
acid sequence of the present protein revealed that the
protein was similar to rice (*Oryza sativa*) hypothetical
20 protein (Accession No. AAD39600). Table 7 shows the
comparison between amino acid sequences of the human protein
of the present invention (HP) and rice hypothetical protein
(OS). Therein, the marks of -, *, and . represent a gap, an
amino acid residue identical with that of the protein of the
25 present invention, and an amino acid residue similar to that

of the protein of the present invention, respectively. The both proteins shared a homology of 40.0% in the intermediate region of 195 amino acid residues.

5 Table 7

HP MTPEDPEETQPLLGPFGGSAPRGR

OS MSFRGEESGGEDGGRTASASDLRKPFLHTGSWYKMSSAGGGGGMGSRGSSAYSRLDSSV

10

HP RVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGG

* .. *****. ***. *.***. *. .. * **.. ..**.*.

OS SAVLCTLIVALGPIQFGFTCGFSSPTQDAI----ISDLGLTLSEFSLFGSLSNVGAMVGA

15

HP VLGGWLVDGRGRKLSLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVY

. . * ... *** **.. ..* . *. .*. *. * .*. ****.*. ** * *,***

OS IASGQIAEYIGRKGSLMIAAIPNIIGWLAISFAKDSSFLFMGRLLLEGFGVGVISYVVPVY

HP ISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPLMLLLMCFMPE

20

*.*** ...** *** ** *..***** * . ** *.*** . * *... . *.**

OS IAEIAPQTMRGALGSVNQLSVTIGILLAYLLGMFVPWRILSVLGILPCSILIPGLFFIPE

HP TPRFLLTQHRRQEAPGLVRCGHGVQHECLRRLLQADPGWPWQLLARGHLGACLCTAC

.**.*..*. *

25

OS SPRWLAKMGKMEDFESSLQVLRGFETDIAVEVNEIKRSVQSSRRRTTIRFADIKQKRYSV

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW028826) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10786> (SEQ ID NOS: 10, 20, and 30)

Determination of the whole base sequence of the cDNA insert of clone HP10786 obtained from cDNA library of human kidney revealed the structure consisting of a 78-bp 5'-untranslated region, a 459-bp ORF, and a 585-bp 3'-untranslated region. The ORF encodes a protein consisting of 152 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 10 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 17 kDa that was almost identical with the molecular weight of 16,904 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW052022) among ESTs.

However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03727> (SEQ ID NOS: 31, 41, and 51)

5 Determination of the whole base sequence of the cDNA insert of clone HP03727 obtained from cDNA library of human kidney revealed the structure consisting of a 254-bp 5'-untranslated region, a 1008-bp ORF, and a 355-bp 3'-untranslated region. The ORF encodes a protein consisting of
10 335 amino acid residues and there existed one putative transmembrane domain. Figure 11 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product
15 of 41 kDa that was somewhat larger than the molecular weight of 37,999 predicted from the ORF.

 The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to protein MG87 from diabetic rat
20 kidney (Accession No. AAC64190). Table 8 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and protein MG87 from diabetic rat kidney (RD). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the
25 protein of the present invention, and an amino acid residue

similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 74.2% in the entire region.

5 Table 8

HP MGASSSSALARLGLPARPWPRWLGVAALGLAAVALGTVAWRRRAWPRRRRLQQVGTVAKL
 .*.*****.*. . *****.*****.*****. .
 RD MGSSSSTALARLGLPGQPRSTWLGVAALGLAAVALGTVAWRRRARPRRRQLQQVGTVSKV

10 HP WIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIKEDGHMVTARQEPRLVLISIIYEN
 ****.*****. *. *.***.****. *. *****. *. *****.*****. .*. **
 RD WIYPIKSCGVSVCETECTDMGLRCGKVRDRFWMVVKEDGHMITARQEPRLVLVTITLEN

15 HP NCLIFRAPDMDQLVLPSPKQPSSNKLHNCRIFGLDIKGRDCGNEAAKWFTNFKTEAYRLV
 .. . *. *. . .*** * *****. *. **. *****. *. *.***. .***.*****
 RD NYLMLEAPGMEPIVLPIKLPSSNKIHDCRLFGLDIKGRDCGDEVARWFTSYLKTQAYRLV

HP QFETNMKGRTSRKLLPTLD--QNFQVAYPDYCPLLIMTDASLVDLNRMEKKMKMENFRP
 20 **. *.*****. ** *. . **. *****. *. . . .*****. **.*** **
 RD QFDTKMKGRTTKKLYPSESYLQNYEVAYPDCSPIHLISEASLVDLNLRLQKKVKMEYFRP

HP NIVVTGCDAFEEDTWDELLIGSVEVKVMACPRCILTTPDPTGVDRKQPLDTLKSRYL
 ****. **. *****. **. *. *. .****. *****. ****. **. *****
 25 RD NIVVSGCEAFEEDTWDELLIGDVEMKRVLSCPRCVLTPDPTGII DRKEPLETLKSRYL

HP CDPSERELYKLSPLFGIYYSVEKIGSLRVGDPVYRMV

**** ..** *****.* *****

RD CDPSVKSLYQSSPLFGMYFSVEKIGSLRVGDPVYRMVD

5

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI912794) among ESTs. However, since they are
10 partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03801> (SEQ ID NOS: 32, 42, and 52)

Determination of the whole base sequence of the
15 cDNA insert of clone HP03801 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 158-bp 5'-untranslated region, a 627-bp ORF, and a 964-bp 3'-untranslated region. The ORF encodes a protein consisting of 208 amino acid residues and there existed six
20 putative transmembrane domains. Figure 12 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 23 kDa that was almost identical with the molecular
25 weight of 22,526 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human hypothetical protein CGI-15 (Accession No. AAD27724). Table 9 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human hypothetical protein CGI-15 (CP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The amino acid sequences of the two proteins were completely different each other in the N-terminal, intermediate and C-terminal regions although partial match was observed.

Table 9

HP	MELRAALVLVLLIAGGLFMFTYKSTQFNVEGFALVLGASFIGGIRW
	***** *.. ..
CP	VLFILIFSLIFKLEELRAALVLVLLIAGGLFMFTYKSTQFNVEGFAWCWGRSSVAFAG
HP	TLTQMLLQKAEGLQNPIDTMFHLQPLMFLGLFPLFAVFEGLHLSTSEKIFRQDTGLLL
 * .. *****
CP	PSPRCSCRRLNSASRIPSTPCSTCSHSCSWGFLFPLFAVFEGLHLSTSEKIFRQDTGLLL
HP	RVLGSLFLGGILAFGLGFSEFLVSRSSLTLSIAGIFKEVCTLLLAHLLGDQISLLNW

CP RVLGSLFLGGILAFGLGFSEFLVSRSTSLTSLIAGIFKEVCTLLAAHLLGDQISLLNW

HP LGFALCLSGISLHVALKALHSRGNPESLPEASVFCSSPCDS

5 *****

CP LGFASASREYPSTLPSKPCIPEVMVAPRP

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI741613) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

15 <HP03883> (SEQ ID NOS: 33, 43, and 53)

Determination of the whole base sequence of the cDNA insert of clone HP03883 obtained from cDNA library of human kidney revealed the structure consisting of a 59-bp 5'-untranslated region, a 1221-bp ORF, and a 122-bp 3'-untranslated region. The ORF encodes a protein consisting of 406 amino acid residues and there existed eight putative transmembrane domains. Figure 13 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product

of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human choline/ethanolamine phosphotransferase (Accession No. NP_006081). Table 10 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human choline/ethanolamine phosphotransferase (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 66.8% in the entire region. In addition, the amino acid sequence from position 70 to position 311 of the present protein shared a homology of 98.3% with human AAPT1-like protein (Accession No. AAD44019).

Table 10

20	HP	MAAGAGAGSAPRWLRALSEPLSAAQLRRLEEHRYSAG
		*** **.*****.**
	CE	MSGHRSTRKRCGDSPVGFHMTGCVLNKLFQLPTPLSRHQLKRLEEHRYSAG
	HP	VSLLEPPLQLYWTWLLQWIPLWMAPNSITLLGLAVNVVTTLVLSYCPTATEEAPYWTYL
25		*****.* **.*. ...* *.*** **..**..*. **..*. *****.**.*.

*****, *****, **, *** **

HP WFFFCFIGMFV FYCAHWQTYVSGMLRFGKVDVTEIQIALVIVFVLSAFGGATMWDYTIP

*.***.* * * *.*****.*****.*. *. *.***.*. **

10

HP ILEIKLKILPVLGFLGGVIFSCSNYFHVILHGGVGKNGSTIAGTSVLSPLHIGLIITLA

. * . * . * . * . * . * . * . * . * . * . * . * . *

CE VLNIQM KIFPALCTVAGTIF SCTNYFRVIFTGGVGKNGSTIAGTSVLSPFLHIGSVITLA

15 HP IMIYKKSATDVFEKHPCLYILMFGCVFAKVSQKLVAHMTKSELYLQDTVFLGPGLFLD

*****.***** ** * *.*****.*****.*****

CE AMIYKKS AVQLFEKHPCLYILTFGFVSAKITNKL VVAHMTKSEMHLHDTAFIGPALLFLD

HP QYFNNFIDEYVVLWMAMVISSFDMVIYFSALCLQISRHLHLNIFKTACHQAPEQVQVLSS

20 ****.*****.***.*.*.* **.. * ..* **..***...*

CE QYFNSFIDEYIVLWIALVFSFFDLIRYCVSVCNQIASHLHIHVFRIKVSTAHSNHH

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example,

Accession No. AI816449) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5 <HP03913> (SEQ ID NOS: 34, 44, and 54)

Determination of the whole base sequence of the cDNA insert of clone HP03913 obtained from cDNA library of human kidney revealed the structure consisting of a 344-bp 5'-untranslated region, a 1857-bp ORF, and a 273-bp 3'-
10 untranslated region. The ORF encodes a protein consisting of 618 amino acid residues and there existed thirteen putative transmembrane domains. Figure 14 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro
15 translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human solute carrier family 5
20 (Accession No. NP_000444). Table 11 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human solute carrier family 5 (SC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the
25 present invention, and an amino acid residue similar to that

of the protein of the present invention, respectively. The both proteins shared a homology of 48.3% in the entire region.

5 Table 11

HP MEVKNFAVWDYVVF AALFFISSGIGVFFAIKERKKATSREFLVGGRQMSFGPVG
 * .*.*** ** .*.***.*.***. . . .*.***. . . .***
 SC MEAVETGERPTFGAWDYGVFALMLLVSTGIGLWVGLARGGQRSAEDFFTGGRRLAALPVG
 10 HP LSLTASFMSAVTVLGTPSEVYRFGASFLVFFIAYLFVILLTSELFVPFYRSGITSTYEY
 .** ***.***. **. * .** . . . * . **. **. ***** *.*****
 SC LSLSASFMSAVQVLGVPSEAYRYGLKFLWMCLGQLLNSVLTALLFMPVFYRLGLTSTYEY
 15 HP LQLRFNKPVRYAATVIYIVQTIYLTGVVVYAPALALNQVTGFDLWGSVFATGIVCTFYCT
 *.**...** .*. ***,*.****. *.***** *****.*.*.*...***.****.
 SC LEMRFSRAVRLCGTLQYIVATMLYTGIVYIYAPALILNQVTGLDIWASLLSTGIICTFYTA
 HP LGGLKAVVWTDADFQMVVMIVGFLTVLIQGSTHAGGFHNVLEQSTNGSRLHIFDFDVPDLR
 20 *.*****.***.***. ** .** .* .** ...** . * **...** .** .
 SC VGGMKAVVWTDVDFQVVVMLSGFWVVLARGVMLVGGPRQVLTLAQNHSRINLMDFNPDPRS
 HP RHTFWTITVGCTFTWLGIYGVNQSTIQRCSCKTEKHAKLALYFNLLGLWIILVCAVFSG
 *.****.****.***.*****. **.***.***.***** .* .**.*. .*. .*
 25 SC RYTFWTFVVGGLVWLSMYGVNQAVQRYVACRTEKQAKLALLINQVGLFLIVSSAACCG

HP LIMYSHFKDCDPWTSGIISAPDQLMPYFVMEIFATMPGLPGLFVACAFSGTLSTVASSIN
..*. ..**** * ***** ** .*.**...*.****.***.*****...***
SC IVMFVFTDCDPLLLGRISAPDQYMPLLVLDIFEDLPGVPGLFLACAYSGTLSTASTSIN
5
HP ALATVTFEDFVKSCFPHLSDKLSTWISKGLCLLFGVMCTSMAVAASVM-GGVVQASLSIH
*.**.* **..* . . * . . . *****.*.* * ..* .*. .***.*.*..
SC AMAAVTVEDLIKPRRLSLAPRKLVIISKGLSLIYGSACLTVAALSSLLGGGVLQGSFTVM
10
HP GMC GG PMLGLFSLGIVFPFVNWKALGGLLTGITLSFWAIGAFIYPAPASKTWPLPLST
*. **. ** * **. . * * *.**.*.***.***.***... . ** *.
SC GVISGPLLGAFILGMFLPACNTPGVLAGLGAGLALSLWVALGATLYPPSEQTMRVLPSSA
HP DQCIKSNVTATG---PPVL-----SSRPGIADTWYSISYLYYSAVGCLGCI
15
..*. .*.** * ..* .***.***.*.***.***.*.*. .
SC ARCVALSVNASGLLDPALLPANDSSRAPSSGMDASRPALADSFYAISYLYYGALGTLTTV
HP VAGVIISLITGRQRGEDIQPLLIRPVCNLCFWSKKYKTLWCQGVQHDSGTEQENLENGS
.*.***.***.* *..
20
SC LCGALISCLTGPTKRSTLAPGLLWDLARQTASVAPKEEVAILDDNLVKGPPELPTGNKK
HP ARKQGAESVLQNGLRRESLVHVPGYDPKDKSYNNMAFETTHF
SC PPGFLPTNEDRLFFLGQKELEGAGSWTPCVGHDGGRDQQETNL
25

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI733508) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10753> (SEQ ID NOS: 35, 45, and 55)

Determination of the whole base sequence of the cDNA insert of clone HP10753 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 141-bp 5'-untranslated region, a 627-bp ORF, and a 2528-bp 3'-untranslated region. The ORF encodes a protein consisting of 208 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 15 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 28 kDa that was somewhat larger than the molecular weight of 21,518 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from methionine at position 32.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW162064) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10758> (SEQ ID NOS: 36, 46, and 56)

Determination of the whole base sequence of the cDNA insert of clone HP10758 obtained from cDNA library of human kidney revealed the structure consisting of a 25-bp 5'-untranslated region, a 1509-bp ORF, and a 284-bp 3'-untranslated region. The ORF encodes a protein consisting of 502 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 16 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 60 kDa that was somewhat larger than the molecular weight of 55,848 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 66 kDa. In addition, there exists in the amino acid sequence of this protein six sites at which N-glycosylation may occur (Asn-Val-Ser at position 67, Asn-Tyr-Thr at position 103, Asn-

Phe-Thr at position 156, Asn-Ile-Thr at position 183, Asn-Phe-Thr at position 197 and Asn-Lys-Ser at position 283). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from alanine at position 15.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T96740) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10771> (SEQ ID NOS: 37, 47, and 57)

Determination of the whole base sequence of the cDNA insert of clone HP10771 obtained from cDNA library of human kidney revealed the structure consisting of a 36-bp 5'-untranslated region, a 1011-bp ORF, and a 599-bp 3'-untranslated region. The ORF encodes a protein consisting of 336 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 17 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 41 kDa that was somewhat larger than the molecular weight

of 37,924 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human interferon- α induced protein (Accession No. AR053364). The C-terminal portion downstream from methionine at position 51 of the protein of the present invention matched with the C-terminal portion downstream from methionine at position 12 of human interferon- α induced protein. However, the putative transmembrane domain at the N-terminus observed for the protein of the present invention was not present in human interferon- α induced protein.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA452543) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10778> (SEQ ID NOS: 38, 48, and 58)

Determination of the whole base sequence of the cDNA insert of clone HP10778 obtained from cDNA library of human kidney revealed the structure consisting of a 173-bp 5'-untranslated region, a 1023-bp ORF, and a 220-bp 3'-untranslated region. The ORF encodes a protein consisting of 340 amino acid residues and there existed six putative

transmembrane domains. Figure 18 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA429745) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10781> (SEQ ID NOS: 39, 49, and 59)

Determination of the whole base sequence of the cDNA insert of clone HP10781 obtained from cDNA library of human kidney revealed the structure consisting of a 88-bp 5'-untranslated region, a 672-bp ORF, and a 1167-bp 3'-untranslated region. The ORF encodes a protein consisting of 223 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 19 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 31 kDa that was larger than the molecular weight of 24,239 predicted from the ORF. In this case, the addition of

a microsome led to the formation of a product of 33 kDa. In addition, there exists in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Asn-Thr at position 70 and Asn-Thr-Ser at position 71).

5 Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamine at position 23.

The search of the GenBank using the base sequences
10 of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA334609) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present
15 invention.

<HP10785> (SEQ ID NOS: 40, 50, and 60)

Determination of the whole base sequence of the cDNA insert of clone HP10785 obtained from cDNA library of human kidney revealed the structure consisting of a 171-bp
20 5'-untranslated region, a 930-bp ORF, and a 318-bp 3'-untranslated region. The ORF encodes a protein consisting of 309 amino acid residues and there existed six putative transmembrane domains. Figure 20 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-
25 Doolittle method, of the present protein. In vitro

translation resulted in formation of a translation product of high molecular weight.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI822041) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

10 <HP03878> (SEQ ID NOS: 61, 71, and 81)

Determination of the whole base sequence of the cDNA insert of clone HP03878 obtained from cDNA library of human kidney revealed the structure consisting of a 77-bp 5'-untranslated region, a 1800-bp ORF, and a 139-bp 3'-untranslated region. The ORF encodes a protein consisting of 599 amino acid residues and there existed ten putative transmembrane domains. Figure 21 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to flounder (*Pseudopleuronectes americanus*) Na/Pi cotransport system protein (Accession No.

AAB16821). Table 12 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and flounder Na/Pi cotransport system protein (PN). Therein, the marks of -, *, and . represent a gap, an amino acid
5 residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 57.1% in the region of 545 amino acid residues other than the N-terminal and C-terminal
10 regions.

Table 12

HP MPSSLPGSQVPHPTLDAVDLVEKTLRNEGTSAPVLEEGDTPWTLPLKDTSQPWKEL

* .. *.***. *. * .. *.**

PN MAPRQKVGNTSSPKPALDDAPVGNIPPAYSTLDLVSDPDADPWNAPELIDNGVKWSEL

HP RVAGRLRRVAGSVLKACGLLGSLYFFICSLDLSSAFQLLGSKVAGDIFKDNVLSNPVA

. *... ** ... ** . *** *****. *. *. *****. **. ****

PN DTKGKMMRVLTGLLKLVALLGLLYFFICSLDLSSAFQLVGGKAAGDIFKDNVLANPVA

HP GLVIGVLVTALVQSSSTSSSIIVSMVAAKLLTVRVSVPIIMGVNVGTSITSTLVMAQSG

*****. . *****. . **. *. . *****. *. ***. *. *. * * *

PN GLVIGVLVTVMVQSSSTSSSIIVSMVSSGLLDVQSAVPIIMGANIGTSVTNTIVAMMQAG

HP DRDEFQRAFSGSAVHGIFNWLTVLVLLPLESATALLERLSELALGAASLTPRAQAPDILK

.. **. *. *. * .. ****. **. ***** **. * . *. * * ***. *

PN DRNEFRRAFAGATVHDFFNWLAVLILLPLEVATGVLYKLTHLIIESFNIQGGEDAPDLLN

HP VLTkPLTHLIVQLDSDMI—MSSATGNATNSSLIKHWCGTTGQPT—QENSSCGAFGPC

*. *. ***. *****... * *. * ****. ** *... * *. * . *

PN VITDPLTDSIVQLDKNVISLIATNDEAAVNMSLIKEWCKTKTNVTFWNATVENCTAGALC

HP TEKNSTA————PADRLPCRHLFAGTELTLAVGCILLAGSLLVLCGCLVIVKLLN

*... . .. *. *. ** *. * ***** **** **. ***. **. *****

PN WEEGNLTWTMLNKTWIIINQERCKHIFANTTLPDLAVGLILLALSFLVLTCLILIVKLLN

HP SVLRGRVAQVVRTVINADFPFPLGWLGGYLAVLAGAGLTFALQSSSVFTAADVPLMGVGV
*. *. *. ** *. ***. ****. *. *. *. ***. ** . ****. *. *. *. **

PN SMLKGQVAVVIKRVINTDFPFPFCWVTGYIAIFVGAGMTFIVQSSSVFTSAITPLVGIGV

HP ISLDRAYPLLLGSNIGTTTTALLAALASPADRMLSALQVALIHFFFNLAGILLWYLVPA
. *. ****. ****. ***. ****. *. ** ****. ****. * . *

PN ISLERAYPLTLGSNIGTTTTAILAAMASPAEKLKESLQIALCHFFFNVMGILLFYPIPFT

HP RLPIPLARHFGVVTARYRWVAGVYLLLGFLLLPLAAFGLSLAGGMVLAAGGPLVGLVLL
*. *. *** . * *. *** ** *. * *. *. *. *. ****. ** *. *. * . * . *

PN RVPIRLARGLGNHTAKYRWFAGLYLVLCFLVFPLTVFGLSMAGWQVLVGVGVPFVVLIVF

HP VILVTVLQRRRPAWLPVRLRSWAWLPVWLHSLEPWDRLVTRCCPCNVCSPPKATTKEAYC
** *. *. *. * * . ** *. *. * . ** ***. *** . **

PN VIVVNVMSRCPRFLPKVLQDWFPLPRPLHSMAPWDTVVTSALGFCGKYCCCCCKCKKT

HP YENPEILASQQL

PN EDENMMKNNTKSLEMYDNPSMLKDEDTKEASKATHL

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792826) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03884> (SEQ ID NOS: 62, 72, and 82)

Determination of the whole base sequence of the cDNA insert of clone HP03884 obtained from cDNA library of human kidney revealed the structure consisting of a 336-bp 5'-untranslated region, a 246-bp ORF, and a 864-bp 3'-untranslated region. The ORF encodes a protein consisting of 81 amino acid residues and there existed one putative transmembrane domain. Figure 22 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa that was almost identical with the molecular weight of 8,928 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to rat cortexin (Accession No. P41237). Table 13 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and rat

cortexin (RC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 47.9% in the entire region.

Table 13

```

HP  MDGGQPIPSSLVPLGNESADSSMSLEQKMTFVFVILLFIFLGILIVRCFRILLDPYRSM
10      *..* * .. .....** .*.**. *. * .*.*** *****..*
RC  MSAPWTLSPEPLPPSTGPPVGAGLDVEQRTVFAFVLCLLVVLVLLMVRCVRILLDPYSRM

HP  PTSTWADGLEGLEKGQFDHALA
      *. *. *. * *. **. ****. **
15 RC  PASSWTDHKEALERGQFDYALV

```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI791379) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03934> (SEQ ID NOS: 63, 73, and 83)

25 Determination of the whole base sequence of the

cdNA insert of clone HP03934 obtained from cdNA library of human kidney revealed the structure consisting of a 39-bp 5'-untranslated region, a 1965-bp ORF, and a 463-bp 3'-untranslated region. The ORF encodes a protein consisting of 654 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 23 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 80 kDa that was larger than the molecular weight of 74,110 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from arginine at position 28.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human β -galactosidase (Accession No. AAC12775). Table 14 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human β -galactosidase (BG). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 54.6% in the entire region.

Table 14

HP MAPKKLSCLRSLLLPLSLTLL-----LPQADTRSFVDRGHDRFLLDGAPFRYVSGSLHY

. * *** * * ** * . . * . * * . * . * . * . * . * . * . * . * . * . * . * . *

BG MPGFLVRILLLLVLLLGPTRGLRNATQRMFEIDYSRDSFLKDGQPFYISGSIHY

HP FRVPRVLWADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLL

**** * ***** . ***** ***** . *** ** * . * . . . * . ** . * . **

BG SRVPRFYWKDRLLKMKMAGLNAIQTYVPWNFHEPWPQYQFSEDHDVEYFLRLAHELGLL

HP VILRPGPYICAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNG

***** . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *

BG VILRPGPYICAEWEMGGLPAWLEKESILLRSSDPDYLAAVDKWLGVLPPKMKPLLYQNG

HP GNIISIQVENEYGSYRACDFSVMRHLAGLFRALLGEKILLFTTDGPE--GLKCGSLRGLY

* . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *

BG GPVITVQVENEYGSYFACDFDYLRLQKRFRHHLGDDVVLFTTDGAHKTFKCGALQGLY

HP TTVDFGPADNMTKIFTLLRKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKLENML

***** . . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *

BG TTVDFGTGSNITDAFLSQRKCEPKGPLINSEFYTGWLDHWGQPHSTIKTEAVASSLYDIL

HP KLGASVNMVMFHGGTNFGYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVIS

***** . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *

BG ARGASVNLVYFVGGTNFAYWNGAN--SPYAAQPTSVDYDAPLSEAGDLTEKYFALRNI IQ

HP KFQEVPLGPLPPSPKMMLGPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGF

**. ** **. **. **. * *. . . * *. *. *. *. *. *. *. *. *. *

BG KFEKVPEGPIPPSTPKFAYGKVTLKLTVGAAALDILCPSPGIKSLYPLTFIQVKQHYGF

HP MLYRTYMTHTIFEPTPFWVPNNGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDI

. **** . . . *. *. * ***** *. *. *. *. *. *. *. *. *

BG VLYRTTLPQDCSNPAPLSSPLNGVHDRAYVAVDGIPQGVLERNNVITLNTGKAGATLDL

HP LVENMGRLSFGSNSSDFKGLLKPPILGQTILTQWMMFPLKIDNLVK-----W--W-FPLQ

*****. *. . *****. *. *. *. *. *. *. *. *

BG LVENMGRVNYGAYINDFKGLVSNLTLSSNILDWTIFPLDTEDAVRSHLGGWGHDRDSGH

HP LPKWYPYPQAP-SGPTFYSKTFPILGSVD-----TFLYLPGWTKGQVWINGFNLGRYWTQ

*. . . *. *. *. *. *. * *. . *****. .

BG DEAWAHNSSNYTLPAFYMGNFSPSGIPDLPQDTFIQFPGWTKGQVWINGFNLGRYWP

HP GPQQTLYVPRFLLFPRGALNKITLLELE-----DVPLQPQVQFLDKPILNSTSTLHRT

*** *. *. *. *. . . *. *. *. *. * * . * *. *. *. *. *. *

BG GPQLTLFVPQHILMTSAP-NTITVLELEWAPCSSDDPELCAVTFVDRPVIGSSVTYDHP

HP INSLSADTLSASEPMELSGH

BG KPVEKRLMPPPPQKNKDSWLDHV

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI907720) among ESTs. However, since they are
5 partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03949> (SEQ ID NOS: 64, 74, and 84)

Determination of the whole base sequence of the
10 cDNA insert of clone HP03949 obtained from cDNA library of human kidney revealed the structure consisting of a 244-bp 5'-untranslated region, a 1173-bp ORF, and a 33-bp 3'-untranslated region. The ORF encodes a protein consisting of 390 amino acid residues and there existed ten putative
15 transmembrane domains. Figure 24 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

20 The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human solute carrier family 16 (Accession No. NM_004696). Table 15 shows the comparison between amino acid sequences of the human protein of the
25 present invention (HP) and human solute carrier family 16

(HS). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The
5 both proteins shared a homology of 98.7% in the region other than the N-terminal and C-terminal regions.

Table 15

HP MGDDDCDSFFPGPLVAIICDILGEKTTSSILGAFVVTGGYLISWATSIPFLCVTMGLL
 * . *****
 HS WIGSIMSSLRFCAGPLVAIICDILGEKTTSSILGAFVVTGGYLISWATSIPFLCVTMGLL

 HP PGLGSAFLYQVAAVVTTKYFKKRLALSTAIARSGMGLTFLAPFTKFLIDLYDWTGALIL

 HS PGLGSAFLYQVAAVVTTKYFKKRLALSTAIARSGMGLTFLAPFTKFLIDLYDWTGALIL

 HP FGAIALNLPSSMLLRPIHIKSENNSGIKDKGSSLSAHGPEAHATETHCHETEESTIKDS

 HS FGAIALNLPSSMLLRPIHIKSENNSGIKDKGSSLSAHGPEAHATETHCHETEESTIKDS

 HP TTQKAGLPSKNLTVSQNQSEEFYNGPNRNRLLKSDEESDKVISWSCKQLFDISLFRNPF

 HS TTQKAGLPSKNLTVSQNQSEEFYNGPNRNRLLKSDEESDKVISWSCKQLFDISLFRNPF

 HP FYIFTWSFLLSQLAYFIPTFHLVARAKTLGIDIMDASYLVSVAGILETVSQIISGWVADQ

 HS FYIFTWSFLLSQLAYFIPTFHLVARAKTLGIDIMDASYLVSVAGILETVSQIISGWVADQ

 HP NWIKKYHYHKSYLILCGITNLLAPLATTFPLLMTYITICFAIFAGGYLALILPVLVDLCRN

 HS NWIKKYHYHKSYLILCGITNLLAPLATTFPLLMTYITICFAIFAGGYLALILPVLVDLCRN

 HP STVNRFLGLASFFAGMAVLSGPPIAGNTFTTF

 HS STVNRFLGLASFFAGMAVLSGPPIAGWLYDTQTYNCSFYFSGICYLLSSVSFFVPLAE

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW239415) among ESTs. However, since they are
5 partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03959> (SEQ ID NOS: 65, 75, and 85)

Determination of the whole base sequence of the
10 cDNA insert of clone HP03959 obtained from cDNA library of human kidney revealed the structure consisting of a 7-bp 5'-untranslated region, a 1359-bp ORF, and a 531-bp 3'-untranslated region. The ORF encodes a protein consisting of 452 amino acid residues and there existed a putative
15 secretory signal at the N-terminus. Figure 25 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 53 kDa that was somewhat larger than the molecular weight
20 of 50,798 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 55 kDa. In addition, there exists in the amino acid sequence of this protein three sites at which N-glycosylation may occur (Asn-Phe-Ser at position 64, Asn-Gly-Ser at position 126 and Asn-
25 Val-Thr at position 362). Application of the (-3,-1) rule, a

method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from alanine at position 27.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Arabidopsis thaliana* putative carboxypeptidase (Accession No. AAD21510). Table 16 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Arabidopsis thaliana* putative carboxypeptidase (AC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 44.3% in the region of 323 amino acid residues other than the N-terminal and C-terminal regions.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T59065) among ESTs. However, since they are
5 partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03983> (SEQ ID NOS: 66, 76, and 86)

Determination of the whole base sequence of the
10 cDNA insert of clone HP03983 obtained from cDNA library of human kidney revealed the structure consisting of a 42-bp 5'-untranslated region, a 1473-bp ORF, and a 341-bp 3'-untranslated region. The ORF encodes a protein consisting of 490 amino acid residues and there existed a putative
15 secretory signal at the N-terminus and one putative transmembrane domain at the C-terminus. Figure 26 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. Application of the (-3,-1) rule, a method for predicting the cleavage
20 site of the secretory signal sequence, allows to expect that the mature protein starts from glutamic acid at position 22.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human ClqR protein (Accession No.
25 AAB53110). Table 17 shows the comparison between amino acid

sequences of the human protein of the present invention (HP) and human ClqR protein (HC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 25.8% in the N-terminal region of 310 amino acid residues. Since the positions of 17 cysteine residues are conserved, in particular, the two proteins are considered to assume similar higher-order structures.

Table 17

HP MRPALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAABEACILRGGA
 * * ** * . ** . * * * *
 HC MATSMGLLLLLLLLLLTQPGAGTGADTEAVVC-VGTACYTAHSGKLSAAEAQNHCNQNGGN

 HP LSTVRAGAE LRAVLALL--RAGPGPGGGSKD LFWVALERRRSHCTLENEPLRGFSWLSS
 * . ** . . * . * ** . * . * . * ** . **** .
 HC LATVKSKEEAQHVRVLAQLLRREAAALTARMSKFWIGLQREKKGKCLDPSLPLKGF SWV--

 HP DPGGLESDTLQWVEPQRSCTARRC--AVLQATGGVEP--AGWKEMRC-----HLRAN
 ** . . . * . * . . . ** * . . . * . * . * . * . . .
 HC -GGGEDTPYSNWHKELRNSCISKRCVSLLLDLSQPLLPNRLPKWSEGPCGSPGSPGSNIE

 HP GYLCKYQFEVLCAPRPGAASNLSYRAPFQLHSAALDFSPPGTEVSALC-----RGQLPIS
 * . ** . * . * . . * * * *
 HC GFVCKFSFKGMCRLALGGPGQVTTYTPFQTTSSSLEAVPFASAANVACGEGDKDETQSH

 HP -VTCIADEIGA-RWDKLSGDVLCPCP--GRYL RAGKCAELPNCLD-DLGGFACECATGFE
 * * . * . . ** . * * * . * . * . * .
 HC YFLCKEKAPDVFDWG--SSGPLCVSPKYGCNFNNGGCHQ--DCFEGGDGSFLCGCRPGFR

111

HP LGKDGRSCVTSGEGQPTLGGTGVPTRRPPATATSPVPQRTWPIRVDEKLGETPLVPEQDN

* . * . * .

HC LLDDLVTCASRNPCCSSPCRGGATCVLGPHGKNYTCRCPQGYQLDSSQLDCVDVDECQDS

HP SVTSIPEIPRWGSQSTMSTLQMSLQAESKATITPSGSVISKFNSTSSATPQAFDSSSAV

HC PCAQECVNTPGGFRCECWVGYPGGPGEGACQDVDECALGRSPCAQGCTNTDGSFHCSC

HP VFIFVSTAVVVLVILTMTVLGLVKLCFHESPSSQPRKESMGPPGLESDPEPAALGSSSAH

HC EGYVLAGEDGTQCQDVDECVGPGGPLCDSLCFNTQGSFHCGLPGWVLAPNGVSCTMGPV

HP CTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

HC SLGPPSGPPDEEDKGEKEGSTVPRAATASPTRGEGTPKATPTTSRPSLSSDAPITSAPL

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R51653) among ESTs. However, since they are
5 partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10745> (SEQ ID NOS: 67, 77, and 87)

Determination of the whole base sequence of the
10 cDNA insert of clone HP10745 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 261-bp 5'-untranslated region, a 1179-bp ORF, and a 733-bp 3'-untranslated region. The ORF encodes a protein consisting of 392 amino acid residues and there existed nine
15 putative transmembrane domains. Figure 27 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of
20 sequences that shared a homology of 90% or more (for example, Accession No. R59881) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

25 <HP10775> (SEQ ID NOS: 68, 78, and 88)

Determination of the whole base sequence of the cDNA insert of clone HP10775 obtained from cDNA library of human kidney revealed the structure consisting of a 30-bp 5'-untranslated region, a 1617-bp ORF, and a 287-bp 3'-untranslated region. The ORF encodes a protein consisting of 538 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 28 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 66 kDa that was larger than the molecular weight of 55,133 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from serine at position 23.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA366320) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10782> (SEQ ID NOS: 69, 79, and 89)

Determination of the whole base sequence of the cDNA insert of clone HP10782 obtained from cDNA library of

human kidney revealed the structure consisting of a 70-bp 5'-untranslated region, a 309-bp ORF, and a 1501-bp 3'-untranslated region. The ORF encodes a protein consisting of 102 amino acid residues and there existed three putative transmembrane domains. Figure 29 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI815463) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10787> (SEQ ID NOS: 70, 80, and 90)

Determination of the whole base sequence of the cDNA insert of clone HP10787 obtained from cDNA library of human kidney revealed the structure consisting of a 54-bp 5'-untranslated region, a 1329-bp ORF, and a 912-bp 3'-untranslated region. The ORF encodes a protein consisting of 442 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 30 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product

of 50 kDa that was almost identical with the molecular weight of 50,562 predicted from the ORF. In this case, the addition of a microsomal led to the formation of a product of 56 kDa. In addition, there exists in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Leu-Thr at position 83, Asn-Phe-Thr at position 89, Asn-Ala-Ser at position 113 and Asn-Lys-Ser at position 151).

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to rat PV-1 (Accession No. AAD41524). Table 18 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and rat PV-1 (RP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 61.1% in the entire region.

. * . . . * . * . * . . **. *****. ***. *

*** **..****..**.*.*..**.*..*..**..** *..**..*****

** * * * *****. *. *. **, *. ****, *. , *****, *. , ****, *.

*** * * ** ** * . * *.** *. *. . ***,***,*****. **. *. *

* * * * *

*... ** *** **** *... * ***** , ** * .. . * ** *** , *****

RP LERQLEARKRELEQLRTEVDVRI SALDTCVKAKSLPAIQ-PR LPGPPNPPP IDPASLEE

HP FKRKILESQRPPAGIPVAPSSG

.*** *..*.*

RP FKKRILESQRPPPLVNPVPPSG

5 Furthermore, the search of the GenBank using the
base sequences of the present cDNA has revealed the
registration of sequences that shared a homology of 90% or
more (for example, Accession No. AL041217) among ESTs.
However, since they are partial sequences, it can not be
10 judged whether or not they encode the same protein as the
protein of the present invention.

<HP03977> (SEQ ID NOS: 91, 101, and 111)

Determination of the whole base sequence of the
cDNA insert of clone HP03977 obtained from cDNA library of
15 human kidney revealed the structure consisting of a 35-bp
5'-untranslated region, a 684-bp ORF, and a 1175-bp 3'-
untranslated region. The ORF encodes a protein consisting of
227 amino acid residues and there existed a putative
secretory signal at the N-terminus and one putative
20 transmembrane domain at the C-terminus. Figure 31 depicts
the hydrophobicity/hydrophilicity profile, obtained by the
Kyte-Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
of 29 kDa that was larger than the molecular weight of
25 25,926 predicted from the ORF. Application of the (-3,-1)

rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from leucine at position 30.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human gp25L2 (Accession No. CAA62380). Table 19 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human gp25L2 (GP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 78.5% in the region other than the N-terminal region.

Table 19

HP MAGVGAGPLRAMGRQALLLALCATGAQGLYFHIGETEKRCFIEEIPDETMVIGNYRTQM

* **. * * . *. *****. *****.

GP MRTLLLVLWLATRGs-ALYFHIGETEKKCFIEEIPDETMVIGNYRTQL

HP WDKQKEVFLPSTPGLGMHVEVKDPDGKVLSRQYGSEGRFTFTSHTPGDHQICLHSNSTR

. ***. * . *. ***. ** *****. **. *. *. *****. *****.

GP YDKQREEYQPATPGFGMCVEVKDPEDKVILAREYGSEGRFTFTSHTPGEHQICLHSNSTK

HP MALFAGGKLRVHLDIQVGEHANNYPEIAAKDKLTEQLRARQLLDQVEQIQKEQDYQRYR

.. *****. *****. *. **. *****. *****. ***. *****. ***. *

GP FSLFAGGMLRVHLDIQVGEHANDYAEIPAKDKLSELQLRVRQLVEQVEQIQKEQNYQRWR

HP EERFRLTSESTNQRVLWWSIAQTVILITGIWQMRHLKSFFEAKKLV

***** ***** ** **. *. *****

GP EERFRQTSESTNQRVLWWSILQTLILVAIGVWQMRHLKSFFEAKKLV

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AR052481, U.S. Patent No. 5831052) in patent data. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10649> (SEQ ID NOS: 92, 102, and 112)

Determination of the whole base sequence of the cDNA insert of clone HP10649 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 114-bp 5'-untranslated region, a 1059-bp ORF, and a 1240-bp 3'-untranslated region. The ORF encodes a protein consisting of 352 amino acid residues and there existed one putative transmembrane domain. Figure 32 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 40 kDa that was almost identical with the molecular weight of 39,774 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to Epiphyas postvittana nucleopolyhedrovirus apoptosis inhibitor iap-1 (Accession No. AAD19698). Table 20 shows the comparison between amino

acid sequences of the human protein of the present invention (HP) and Epiphyas postvittana nucleopolyhedrovirus apoptosis inhibitor iap-1 (EP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with
5 that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 40.8% in the C-terminal region of 49 amino acid residues.

Table 20

HP MESGGRPSLCQFILLGTTSVVTAALYSVYRQKARVSQELKGAKKVHLGEDLKSILSEAPG

HP KCVPYAVIEGAVRSVKETLNSQFVENCKGVIQRLTLQEHKMVWNRTHLWDCSKI IHQR

EP MSATSPLYI INVCENAHEVSAEHVFNVLIERHNSFENYPIDNVAFVNSLIINGF

HP TNTVPFDLVPHEGDVAVRVLKPLDSVDLGLETVYEKFHPSIQSFTDVIGHYISGERPK

EP RYQNVDDAVMCEYCSAVIKNWHEDDCVEFVHATLSPYCVYANKIAQÑENFANNLSTNAFL

HP GIQETEMLKVGATLTGVGELVLDNNSVRLQPPKQGMQYYLSSQDFDSSLQRQESSVKLW

EP VTPGKPICVYSRLTHTNARKSTFEDYWPAALQHLVANI SEAGMFHTKLGETACFFCDGR

HP KVLALVFGFATCATLFFILRKQYLQRQERLRKQMQUEEFQEHEAQLLSRAKPEDRESLKS

EP VRDWLPNDPWQRHAIANPQCYFVVCIKGDEFCNAVRQRDELAPLQSVVALEHVSNDENM

HP ACVVCLSSFKSCVFLECGHVCSCTECYRALPEPKKCPICRQAITRVIPLYS

* . ** . . . * . * * * * . ** ** . *** . *** . * . . .

EP ECKICLERQDRTVLLPCRHFVCVMQCYFAL—DNKCPTCRQDVTDFVKIFVV

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T50032) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10779> (SEQ ID NOS: 93, 103, and 113)

Determination of the whole base sequence of the cDNA insert of clone HP10779 obtained from cDNA library of human kidney revealed the structure consisting of a 34-bp 5'-untranslated region, a 393-bp ORF, and a 1949-bp 3'-untranslated region. The ORF encodes a protein consisting of 130 amino acid residues and there existed two putative transmembrane domains. Figure 33 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AL042495) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention. In addition, this gene was mapped on chromosome 9q34 (Accession No. AC001644).

<HP10790> (SEQ ID NOS: 94, 104, and 114)

Determination of the whole base sequence of the cDNA insert of clone HP10790 obtained from cDNA library of human kidney revealed the structure consisting of a 109-bp
5 5'-untranslated region, a 993-bp ORF, and a 53-bp 3'-untranslated region. The ORF encodes a protein consisting of 330 amino acid residues and there existed one putative transmembrane domain. Figure 34 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-
10 Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 34 kDa that was smaller than the molecular weight of 36,642 predicted from the ORF.

The search of the GenBank using the base sequences
15 of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW241940) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present
20 invention.

<HP10793> (SEQ ID NOS: 95, 105, and 115)

Determination of the whole base sequence of the cDNA insert of clone HP10793 obtained from cDNA library of human kidney revealed the structure consisting of a 70-bp
25 5'-untranslated region, a 1053-bp ORF, and a 206-bp 3'-

untranslated region. The ORF encodes a protein consisting of 350 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 35 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 40 kDa that was somewhat larger than the molecular weight of 37,134 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glycine at position 25.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA326569) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10794> (SEQ ID NOS: 96, 106, and 116)

Determination of the whole base sequence of the cDNA insert of clone HP10794 obtained from cDNA library of human kidney revealed the structure consisting of a 146-bp 5'-untranslated region, a 342-bp ORF, and a 899-bp 3'-untranslated region. The ORF encodes a protein consisting of

113 amino acid residues and there existed one putative transmembrane domain. Figure 36 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro
5 translation resulted in formation of a translation product of 14 kDa that was almost identical with the molecular weight of 12,017 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of
10 sequences that shared a homology of 90% or more (for example, Accession No. AI346561) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

15 <HP10797> (SEQ ID NOS: 97, 107, and 117)

Determination of the whole base sequence of the cDNA insert of clone HP10797 obtained from cDNA library of human kidney revealed the structure consisting of a 129-bp 5'-untranslated region, a 570-bp ORF, and a 459-bp 3'-
20 untranslated region. The ORF encodes a protein consisting of 189 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 37 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro
25 translation resulted in formation of a translation product

of 22 kDa that was almost identical with the molecular weight of 21,053 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamine at position 23.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA356938) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention. In addition, this gene was mapped on chromosome 4 (Accession No. AC004067).

<HP10798> (SEQ ID NOS: 98, 108, and 118)

Determination of the whole base sequence of the cDNA insert of clone HP10798 obtained from cDNA library of human kidney revealed the structure consisting of a 25-bp 5'-untranslated region, a 834-bp ORF, and a 247-bp 3'-untranslated region. The ORF encodes a protein consisting of 277 amino acid residues and there existed seven putative transmembrane domains. Figure 38 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was smaller than the molecular weight of

30,685 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H92084) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10800> (SEQ ID NOS: 99, 109, and 119)

Determination of the whole base sequence of the cDNA insert of clone HP10800 obtained from cDNA library of human kidney revealed the structure consisting of a 158-bp 5'-untranslated region, a 825-bp ORF, and a 924-bp 3'-untranslated region. The ORF encodes a protein consisting of 274 amino acid residues and there existed one putative transmembrane domain. Figure 39 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 33 kDa that was somewhat larger than the molecular weight of 31,108 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 45 kDa. In addition, there exists in the amino acid sequence of this protein five sites at which N-glycosylation may occur (Asn-Ile-Thr at position 145, Asn-Ile-Thr at position 151, Asn-

Ile-Thr at position 164, Asn-Ile-Thr at position 183, and Asn-Thr-Thr at position 256).

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA729308) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

10 <HP10801> (SEQ ID NOS: 100, 110, and 120)

Determination of the whole base sequence of the cDNA insert of clone HP10801 obtained from cDNA library of human kidney revealed the structure consisting of a 133-bp 5'-untranslated region, a 1173-bp ORF, and a 510-bp 3'-untranslated region. The ORF encodes a protein consisting of 390 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 40 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation with the addition of microsome resulted in formation of a product of 50 kDa that was larger than the molecular weight of 41,097 predicted from the ORF. In addition, there exists in the amino acid sequence of this protein five sites at which N-glycosylation may occur (Asn-

15

20

25

Leu-Ser at position 108, Asn-Val-Thr at position 169, Asn-Leu-Ser at position 213, Asn-Val-Thr at position 236 and Asn-Gly-Thr at position 307). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamine at position 30.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human A33 antigen (Accession No. NP_005805). Table 21 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human A33 antigen (HA). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 28.7% in the intermediate region of 265 amino acid residues.

Table 21

HP MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWY-TLHGE

. . . *. * . * . * . * * * * .

HA MVGKMWPVLWTLCAVRVTVD AISVETPQDVLRASQGKSVTLPCITYHTSTSS

HP VSSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEK

. . . *. * . * . . . * . . . *

HA REGLIQWDKLLLTHTERVVIWPF SNKNIHG-ELYKNRVSISNNAEQSDASITIDQLTMA

HP DSGPYSCSVNVQDKQKSRGHSIKTLELNLVPPAPPSCLQGVPHGANVTLSQCSPRS

* . * . * . * . . . * . * . * . * . * . * . * . * . * . * . * . * . * .

HA DNGTYECSVSL---MSDLEGNTKSRVRLVLVPPSKPEGIEGETIIGNNIQLTCQSKEG

HP KPAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTL

. * . * . * . . . * . . . * . * . * . * . * . * . * . * . * . * . * .

HA SPTPQYSWKR-YNILNQEQLAQPASGQPVSLKNISTDTS GYYICTSSNEEGTQFCNITV

HP EV-STGPGA AVVAGAVVGT LVGLGLLAGLVLLYHCRGKALEEPANDIKEDAIAPRTL PWP

. * * . . . * . * . * . * . . . * . . . * . . . * .

HA AVRSPSMNVALYVGIAVGVAALIIIGIIYCCCCRGK---DDNTEDKEDARPNREAYEE

HP KSSDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTDGAHPQPI

HA PPEQLRELSREREEDDYRQEEQRSTGRES PDHLDQ

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R33685) among ESTs. However, 5 since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03696> (SEQ ID NOS: 121, 131, and 141)

Determination of the whole base sequence of the 10 cDNA insert of clone HP03696 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 184-bp 5'-untranslated region, a 1188-bp ORF, and a 589-bp 3'-untranslated region. The ORF encodes a protein consisting of 395 amino acid residues and there existed one 15 putative transmembrane domain. Figure 41 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein database using the amino acid sequence of the present protein revealed that the 20 protein was similar to rat cell surface glycoprotein GP42 (Accession No. P23505). Table 22 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and rat cell surface glycoprotein GP42 (RC). Therein, the marks of -, *, and . represent a gap, 25 an amino acid residue identical with that of the protein of

the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 46.1% in the intermediate region of amino acid residues 62-280.

Table 22

HP MSGMEEYTTVSGEVLQRWKIPSFKENQTLMSGAAATVQSRGQYSCSGQVMIIPQTFTQTSE

RC

MLLWMVLLLC

HP TAMVQVQELFPPPVLSAIPSPEPREGSLVTLRCQTKLHPLRSALRLLFSFHKDGH TLQDR

. * * * . * * . * * . * *

RC VSMTEAQELFQDPVLSRLNSSETSD—LLKCTTKVDPNKPASELFYSFYKDNHIIQNR

HP GPHPELCIPGAKEGDSGLYWCEVAPEGGQVQKQSPQLEVRVQAPVSRPVLTLHHGPADPA

. . . * . * . * . * * * * *

RC SHNPLFFISEANEENSGLYQCVDADKGTIQKSDYLDIDLCTSVSQPVLTQLQHEATNLA

HP VGDMVQLLCEAQRGSPPILYSFYLDEKIVGNHSAPCGGTTSLFPVKSEQDAGNYSCEAE

** . * * ** * * * * *

RC EGDVKVFLCETQLGSLPILYSFYMDGEILGEPLAPSGRAASLLISVKAESGKNYSCQAE

HP NSVSRERSEPKKLSLKGSQVLFPTASNWLVPWLPAS—LLGLMVIAAALLVYVRSWRKAGP

* * * * *

RC NKVSRDISEPKKFPLVVSCTASMKSTT—VVIWLPVSCLVGWPWLLRF

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA446524) among ESTs.

5 However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03882> (SEQ ID NOS: 122, 132, and 142)

Determination of the whole base sequence of the
10 cDNA insert of clone HP03882 obtained from cDNA library of human kidney revealed the structure consisting of a 57-bp 5'-untranslated region, a 1653-bp ORF, and a 484-bp 3'-untranslated region. The ORF encodes a protein consisting of 550 amino acid residues and there existed ten putative
15 transmembrane domains. Figure 42 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

20 The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse solute carrier family 22 (cation transporter)-like protein (Accession No. NP_033229). Table 23 shows the comparison between amino acid sequences
25 of the human protein of the present invention (HP) and mouse

solute carrier family 22 (cation transporter)-like protein (MS). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that
5 of the protein of the present invention, respectively. The both proteins shared a homology of 48.9% in the entire region.

Table 23

HP MAFSKLLEQAGGVGLFQTLQVLTFILPCLMIPSQMLLENFSAAIPGHRCWTHMLDN—G

..**...**. * ** ..*..... * * ...* ..**. * ****...***

MS MAFPELLDRVGGLGRFQLFQTVALVTPILWVTTQNMLENFSAAVPHRCWVPLLDNSTSQ

HP SAVSTNMTPKALLTISIPPGPNQGP HQCRRFRQPQWQLDPNATATSWSEADTEPCVDGW

.....*..**..*****. * **** ***** ..*****. **.*. **** **

MS ASIPGDLGPDVLLAVSIPPGPDQPHQCLRFQRPQWQLTESNATATNWSDAATEPCEDGW

HP VYDRSVFTSTIVAKWDLVCSSQGLKPLSQSIFMSGILVGSFIWGLLSYRFRGRKPLSWCC

.*.* *..*****. **.*.*. ****..*****. . * * ****...*.*.

MS VYDHSTFRSTIVTTWDLVCNSQALRPMAQSIFLAGILVGAAVCGHASDRFRGRRRVLTWSY

HP LQLAVAGTSTIFAPTFVIYCGLRFVAAFGMAGIFLSSLTLMVEWTTTSRRAVTMTTVGCA

* ..*.*.*. * *** ..** ..**.* ..**..... *..***..**.. ..

MS LLVSVSGTAAAFMPTFPLYCLFRLLASAVAGVMMNTASLLMEWTSAQGSPLVMTLNLG

HP FSAGQAALGGLAFALRDWRTLQLAASVPFFAISLISWWLPESARWLI IKGKPDQALQELR

** **. *..*...*. ** ****.*. *** .. *****. ** **.****.

MS FSPGQVLTGSAVGVRWRMLQLAVSAPFFLFFVYSWWLPESARWLITVGKLDQGLQELQ

HP KVARINGHK-EAKNLTIEVLMSSVKEEVASAKEPRSVLDLFCVPVLRWRSCAMLVNFSL

..**.*.* *...**.***.*...** ...*. *. *. * ** *. ..*..

MS RVAAVNRRKAEGDTLTMEVLRSAMEEESRDKAGASLGTLLHTPGLRHRTIISMLCWFAF

HP LISYYGLVFDLQSLGRDIFLLQALFGAVDFLGRATTALLSFLGRRTIQAGSQAMAGLAI

...***..***. **..*****. * *** **.* **** *.. ...** *

MS GFTFYGLALDLQALGSNIFLLQALIGIVDFPVKTGSLLLISRLGRRLCQVSFLVLPGLCI

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI242210) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03903> (SEQ ID NOS: 123, 133, and 143)

Determination of the whole base sequence of the cDNA insert of clone HP03903 obtained from cDNA library of human kidney revealed the structure consisting of a 108-bp 5'-untranslated region, a 657-bp ORF, and a 1988-bp 3'-untranslated region. The ORF encodes a protein consisting of 218 amino acid residues and there existed three putative

transmembrane domains. Figure 43 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 26 kDa that was somewhat larger than the molecular weight of 23,487 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse prominin (Accession No. NP_032961). Table 24 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse prominin (MP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 27.6% in the region other than the N-terminal and C-terminal regions.

Table 24

HP MKHTLALLAPLLGLGLGLALSQLAAGATDCKFLGPAEHLTFTPAARARWLAPRVRAPGLL

. * . . . * * * * . .

MP MALVFSALLLLGLCGKISSEGQPAFHNTPCAMNYELPT-TKYETQDTFNAGIV

HP DSLYGTVRRFLSVVQLNPFPSSELVKALL--NELA-SVKVNEVVRYEAGYVCAVIAGLYL

. . ** * . ** . *** * ** . * * * ** . * . ** * . . ** . . * .

MP GPLYKMHIFLNVVQPNDPPLDLIKKLIQKNFDISVDSKEIALYEIGVLICAILGLLFI

HP LLVPTAGLCFCCCRCHRRCGGRVKTEHK-ALACERAALMVFLLLTLLLLIGVVCAFTN

. * . * . * ** *** . . *** . . . * . . * * * . ** . ** . * ** . *

MP ILMPLVGCFFCMCRCCKCGGEMHQKQKQONAPCRRKCLGLSLLVICLLMSLGIYGFVAN

HP QRTHEQMGPSEAMPETLLSLWGLVSDVPQVSTVTPHPHVPL

* . * * *

MP QQTRTRIKGTQKLAKSNFRDFQTLTETPKQIDYVVEQYTNKNAFSDLDGIGSVLGGR

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792608) among ESTs. However, since they are
5 partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03974> (SEQ ID NOS: 124, 134, and 144)

Determination of the whole base sequence of the
10 cDNA insert of clone HP03974 obtained from cDNA library of human kidney revealed the structure consisting of a 41-bp 5'-untranslated region, a 1791-bp ORF, and a 253-bp 3'-untranslated region. The ORF encodes a protein consisting of 596 amino acid residues and there existed twelve putative
15 transmembrane domains. Figure 44 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

20 The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to rabbit (*Oryctolagus cuniculus*) sodium/glucose cotransporter protein (Accession No. AAA66065). Table 25 shows the comparison between amino acid
25 sequences of the human protein of the present invention (HP)

and rabbit sodium/glucose cotransporter protein (OC).
Therein, the marks of -, *, and . represent a gap, an amino
acid residue identical with that of the protein of the
present invention, and an amino acid residue similar to that
5 of the protein of the present invention, respectively. The
both proteins shared a homology of 89.1% in the entire
region.

Table 25

HP M-AANSTSDLHTPGTQLSVADIIVITVYFALNVAVGIWSSCRASRNTVNGYFLAGRDMTW
* *. ***** *. **. ****. **. *****. *****
OC MVADNSTSDPHAPGQLSVTDIVVITVYFALNVAVGIWSSCRASRNTVSGYFLAGRDMTW

HP WPIGASLFASSEGSGLFIGLAGSGAAGGLAVAGFEWNATYVLLALAWFVPIYISSEIVT
*****. *****. *****. *****
OC WPIGASLFGSSEGSGLFIGLAGSGAAGGLAVAGFDWNATYVLLALAWFGAIYISSEIVT

HP LPEYIQKRYGGQRIRMYLSVLSLLSVFTKISLDLYAGALFVHICLGWNFYLSLTILGI
*. *****. *****. *
OC LAEYIQKRFGGQRIRMYLSVLSLLSVFTKISLDLYAGALFVHICLGWNFYLSLTILTI

HP TALYTIAGGLAAVIYTDALQTLIMVVGAVILTIKAFDQIGYGQLEAAYAQAIPSRITAN
*****. ***. *****. ****. **. ****. *****. *****. **
OC TALYTITGGLVAVIYTDALQTLIMVVGAVILAIAKAFHQIDGYGQMEAYARAIPSRITAN

HP TTCHLPRTDAMHMFDPHTGDLPWTGMTFGLTIMATWYWCTDQVIVQRSLSARDLNHAKA

*****. *****. *****. *****. *****

OC TTCHLPRADAMHMFDPYTGDLPWTGMTFGLTIMATWYWCTDQVIVQRSLSARNLNHAKA

HP GSILASYLKMLPMGLIIMPGMISRALFPDDVGCVVPSECLRACGAEVGCSNIAYPKLVME

*****. *****. *****. *****. *****

OC GSILASYLKMLPMGLMIMPGMISRALFPDEVGCVVPSECLRACGAIEGCSNIAYPKLVME

HP LMPIGLRGLMIAVMLAALMSSLTSIFNSSSTLFTMDIWRRLRPRSGERELLLVGRLVIVA

. **. . *****. *****. ***** .. *****.

OC LMPVGLRGLMIAVMMPALMSSLSSIFNSSSTLFTMDIWRRLRPCASERELLLVGRLVIVV

HP LIGVSAWIPVLQDSNSGQLFIYMQSVTSSLAPPVTAVFVLGVFWRRANEQGAFWGLIAG

*****. **. *****. **. **. *****. **

OC LIGVSAWIPVLQGSNGGQLFIYMQSVTSSLAPPVTAVFTLGIFWQRANEQGAFWGLLAG

HP LVVGATRLVLEFLNPAPPCGEPDTRPAVLGSIHYLHFAVALFALSGAVVVAGSLLTPPPQ

*, *****. *****. . *****. . *****. *. ***. *. *****.

OC LAVGATRLVLEFLHPAPPCGAADTRPAVLSQLHYLHFAVALFVLTGAVAVGGSLLTPPPR

HP SVQIENLTWWTLAQDVPLGTKAGDGQTPQKHAFWARVCGFNAILLMCVNIFFYAYFA

. *****. . *. . **. *****. . *****

OC RHQIENLTWWTLTRDLSLGAKAGDGQTPQRYTFWARVCGFNAILLMCVNIFFYAYFA

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI793336) among ESTs. However, since they are
5 partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03978> (SEQ ID NOS: 125, 135, and 145)

Determination of the whole base sequence of the
10 cDNA insert of clone HP03978 obtained from cDNA library of human kidney revealed the structure consisting of a 99-bp 5'-untranslated region, a 1404-bp ORF, and a 705-bp 3'-untranslated region. The ORF encodes a protein consisting of 467 amino acid residues and there existed a putative
15 secretory signal at the N-terminus. Figure 45 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 55 kDa that was somewhat larger than the molecular weight
20 of 52,352 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 57 kDa. In addition, there exists in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Arg-Thr at position 78 and Asn-His-Ser at position 161).
25 Application of the (-3,-1) rule, a method for predicting the

cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from alanine at position 22.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human tubulo-interstitial nephritis antigen (Accession No. BAA84949). Table 26 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human tubulo-interstitial nephritis antigen (TA). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 50.0% in the region other than the N-terminal region.

Table 26

HP MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQ
 *. **.
 TA MWTGYKILIFSyltTEIWMEKQYLSQREVDLEAYFTRNHTVLQGTRFKRAIFQGQYCRNF
 HP DLCCRGRADDCALP-YLG-AICYDLFCNRTVSDCCPDFWDFC---LGVPPFPFP---IQG
 . ** .*. *. *. * . *. **** **. *. *****. **. . **. . * . *
 TA G-CCEDRDDGCVTEFYAANALCYCDKFCDRENSDCCPDYKSFCREEKEWPPHTQPWYPEG
 HP CMHGGRIYPVLGTYWDNCNRCTCQENRQWQCDQEPCLVDPDMIKAINQGNYGWQAGNHS
 * . . . ***. *** ... **. *. *. *** *. *...*. *. *** * *. *.
 TA CFKDGQHYEEGsvIKENCNSCTC-SGQQWKCSQHVCLVRPELIEQVNGDYGWTAQNYSQ
 HP FWGMLDEGIRYRLGTIRPSSSVMMHEIYTVLNPGEVLPTAFEASEKWPNIHEPLDQG
 *****. *. ... ****. **. ... *. *. . * ... **. * ** ***. *. ****
 TA FWGMTLEDGFKFRLGTLPPSLMLLSMNEMTASLPATTDLPEFFVASWKWPGWTHGPLDQK
 HP NCAGSWAFSTAASVSDRVSISLGHMTPVLSQNLSCDTHQQQGCGRGRLDGAWWFLRR
 . **. **. **. *. * *. *. *****. ** **. *. * ***. **. *
 TA NCAASWAFSTASVAADRIAISKGRYTANLSPQNLISCCAKNRHGCNSGSIDRAWWYLK
 HP RGVVSDHCYPFSGRERDEAGPAPPCMMHSRAMGRGKRQATAHCPNSYVNNNDIYQVTPVY
 . **. *. . *. * * **. *****. ** . ***. .. * *** . * *
 TA RGLVSHACYPLF---KDQNA TNNGCAMASRSDGRGKRHATKPCPNNEKSNRIYQCSPPY
 HP RLGSNDKEIMKELMENGVPQALMEVHEDFFLYKGGIYSHTPVSLGRPERYRRHGTHSVKI
 *. **.. *****. *. *****. *. ***** **. ***. *. . . *. **. **. **. *
 TA RVSSNETEIMKEIMQNGPVQAIMQVHEDFFHYKTGIYRHVTSTNKESEKYRKLQTHAVKL

HP TGWGEETLPDGRTLKYWTAANSWGPWGERGHFRIVRGVNECDIESFVLGVWGRVGMEDM

****. ..*. *. *. *****. ***. *. ***. *****. ***.....**... .*

TA TGWGTLRGAQGQKEKFWIAANSWGKSWGNGYFRILRGVNESDIEKLIIAAWGQLTSSDE

HP GHH

5

TA P

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R48402) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

15 <HP10735> (SEQ ID NOS: 126, 136, and 146)

Determination of the whole base sequence of the cDNA insert of clone HP10735 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 370-bp 5'-untranslated region, a 1431-bp ORF, and a 243-bp 3'-untranslated region. The ORF encodes a protein consisting of 476 amino acid residues and there existed ten putative transmembrane domains. Figure 46 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

25 The search of the protein database using the amino

acid sequence of the present protein revealed that the protein was similar to *Caenorhabditis elegans* tetracycline resistance protein-like protein (Accession No. CAA94337). Table 27 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *C. elegans* tetracycline resistance protein-like protein (CP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 51.5% in the intermediate region of 196 amino acid residues.

Table 27

HP MAGSDTAPFLSQADDPDDGPVPGTGLPGSTGNPKSEEPEVPDQEGLQRITGLSPGRSAL

 CP MVNSQQDYI

HP IVAVLCYINLLNYMDRFTVAGVLPDIEQFFNIGDSSSGLIQTVFISSYMLAPVFGYLG
****. **. *****. **. ** ..*****. *. **..** *****
 CP SVTALFVVNLLNYVDRTVAGVLTQVQTYNISDSLGGGLIQTVFLISFMVFSPPVCGYLG

HP RYNRKYLMCGGIAFWSLVTLGSSFIPGEHFWLLLTRGLVGVGEASYSTIAPTLIADLFV
 *.***.* *...* ..****. *.****. *. *.**.* *****. **. **. *. *
 CP RFNRKWIMIIGVGIWLGAVLGSSFPANHFVFLVLRSFVGIGEASYSNVAPSLISDMFN

HP ADQRSRMLSIFYFAIPVGSGLGYIAGSKVKDMAGDWHWALRVTPGLGVVAVLLLFLVRE
 ...** .. *****. *. **. * ... *. *. *.**.. *..... * * . *
 CP GQKRSTVFMIFYFAIPVGSGLGFIVGSNVATLTGHWQWGIRVSAIAGLIVMIALVLFTYE

HP PPRGAVERHSDLPPLNPTSWWADLRALARNLIFGLITCLTGVLGVLGVEISRRLRHSNP
 * ***...

CP PERGAADKAMGESKDVVVTTNTTYLEDLVILLKTPTLVACTWGYTALVFVSGTLSWWEPT

HP RADPLVCATGLLGSAPFLFSLACARGSIVATYIFIFIGETLLSMNWAIVADILLYVVIP

CP VIQHLTAWHQGLNDTKDLASTDKDRVALYFGAITTAGGLIGVIFGSMLSKWL VAGWGPF

HP TRRSTAEAFQIVLSHLLGDAGSPYLIGLISDRLRRNWPPSFLSEFRALQFSLMLCAFVGA

CP RLQTDRAQPLVAGGGALLAAPFLIGMIFGDKSLVLLYIMIFGITMCFNWGLNIDMLT

HP LGGAFLGTAIFIEADRRRAQLHVQGLLHEAGSTDDRIVVPQGRSTRVPVASVLI

CP TVIHPNRRSTAFSYFVLVSHLFGDASGPYLIGLISDAIRHGSTYPKDQYHSLVSATYCCV

5 The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of
sequences that shared a homology of 90% or more (for example,
Accession No. AA460778) among ESTs. However, since they are
partial sequences, it can not be judged whether or not they
10 encode the same protein as the protein of the present
invention. Furthermore, the search has revealed the
registration of sequences that shared a homology of 90% or
more (Accession No. E12646) in patent data. However, since
they are partial sequences, it can not be judged whether or
15 not they encode the same protein as the protein of the
present invention.

<HP10750> (SEQ ID NOS: 127, 137, and 147)

Determination of the whole base sequence of the
cDNA insert of clone HP10750 obtained from cDNA library of
20 human umbilical cord blood revealed the structure consisting
of a 262-bp 5'-untranslated region, a 1350-bp ORF, and a
564-bp 3'-untranslated region. The ORF encodes a protein
consisting of 449 amino acid residues and there existed four
putative transmembrane domains. Figure 47 depicts the
25 hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, 5 Accession No. AW304031) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10777> (SEQ ID NOS: 128, 138, and 148)

10 Determination of the whole base sequence of the cDNA insert of clone HP10777 obtained from cDNA library of human kidney revealed the structure consisting of a 15-bp 5'-untranslated region, a 318-bp ORF, and a 1030-bp 3'-untranslated region. The ORF encodes a protein consisting of 15 105 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 48 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product 20 of 14 kDa that was somewhat larger than the molecular weight of 11,603 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glycine at position 30.

25 <HP10780> (SEQ ID NOS: 129, 139, and 149)

Determination of the whole base sequence of the cDNA insert of clone HP10780 obtained from cDNA library of human kidney revealed the structure consisting of a 226-bp 5'-untranslated region, a 246-bp ORF, and a 571-bp 3'-untranslated region. The ORF encodes a protein consisting of 81 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 49 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa that was somewhat larger than the molecular weight of 8,533 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 6 kDa. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glycine at position 25.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA658245) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10795> (SEQ ID NOS: 130, 140, and 150)

Determination of the whole base sequence of the cDNA insert of clone HP10795 obtained from cDNA library of human kidney revealed the structure consisting of a 356-bp 5'-untranslated region, a 1659-bp ORF, and a 420-bp 3'-untranslated region. The ORF encodes a protein consisting of 552 amino acid residues and there existed one transmembrane domain at the N-terminus. Figure 50 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 65 kDa that was almost identical with the molecular weight of 64,280 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human UDP-N-acetyl- α -D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (Accession No. NP_004472). Table 28 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human UDP-N-acetyl- α -D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GA). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 49.9% in the entire

156

HP FRKKHPYVFPDGNANTYIKNTKRTAEVWMDEYKQYYAARPFALERPFGNVESRLDLRKN

..**.*. **. *. *****. **** * * . *.**..***.***.

GA FRKQHPYTFPGSGTVFARNTRRAAEVWMDEYKNFYAAVPSARNVPYGNISRLRLRKK

HP LRCQSFKWYLENIYPELSIPKESSIQKGNIRQRQKCLESQRQNNQETPNLKLSPCAKVGK

5 *.**..*****.****..**..*. *.**..**..* *

GA LSCKPFWYLENVYPELRVPDHQDIAFGALQQGTNCLDTLGHFADGVVG---VYEC---H

HP EDAKSQVWAFTYTQILQEELCLSVITLFPGAPVVLVLCKNGDDRQQWTK---TGSHEHI

. . . . * **.* ***.*. **. . * *.**.*.***. . . . *.

GA NAGGNQEWALTKEKSVKHMCLCLTVVDRAPGSLIKLQGCRENDSRQKWEQIEGNSKLRHV

10

HP ASHLCLDMDMGDGTENGKEIVVNPCESSLMSQHWDMVSS

.*.****. *. . . . *. *.**.* **.*

GA GSNLCLDS---R---TAKSGGLSVEVCGPAL-SQQWKFTLNLQQ

15

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA160076) among ESTs. However, since they are partial sequences, it can not be judged whether or not they

20 encode the same protein as the protein of the present invention.

INDUSTRIAL APPLICABILITY

The present invention provides human proteins

25 having hydrophobic domains, DNAs encoding these proteins,

expression vectors for these DNAs and eukaryotic cells expressing these DNAs. Since all of the proteins of the present invention are secreted or exist in the cell membrane, they are considered to be proteins controlling the proliferation and/or the differentiation of the cells. Accordingly, the proteins of the present invention can be employed as pharmaceuticals such as carcinostatic agents which act to control the proliferation and/or the differentiation of the cells, or as antigens for preparing antibodies against these proteins. The DNAs of the present invention can be utilized as probes for the genetic diagnosis and gene sources for the gene therapy. Furthermore, the DNAs can be utilized for expressing these proteins in large quantities. Cells into which these genes are introduced to express these proteins can be utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like. The antibody of the present invention can be utilized for the detection, quantification, purification and the like of the protein of the present invention.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include

contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, 5 promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for 10 identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

15 Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind 20 and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, Trends Pharmacol. Sci. 15(7): 250-254; Lavarosky et al., 1997, Biochem. Mol. Med. 62(1): 11-22; and Hampel, 1998, Prog. Nucleic Acid Res. Mol. Biol. 58: 1-39; all of which are incorporated by reference herein). 25 Transgenic animals that have multiple copies of the gene(s)

corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided.

5 Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms

10 are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s).

15 Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, Bioessays 14(9): 629-633; Zwaal et al., 1993, Proc. Natl. Acad. Sci. USA 90(16): 7431-7435; Clark et al., 1994, Proc. Natl. Acad. Sci.

20 USA 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour et al., 1988, Nature 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153;

25 5,614, 396; 5,616,491; and 5,679,523; all of which are

incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where

sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein
5 fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment
10 of any of the disclosed proteins.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that
15 of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide, as determined by those of skill in the art. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a
20 suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are
25 identical, homologous, or related to that encoded by the

polynucleotides.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

5 The present invention also includes polynucleotides capable of hybridizing under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency
10 conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for
15 example, conditions M-R.

Table 29

Stringency Condition	Poly-nucleotide Hybrid	Hybrid Length (bp) [†]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
A	DNA : DNA	≥50	65°C; 1×SSC -or- 42°C; 1×SSC, 50% formamide	65°C; 0.3×SSC
B	DNA : DNA	<50	T _B *; 1×SSC	T _B *; 1×SSC
C	DNA : RNA	≥50	67°C; 1×SSC -or- 45°C; 1×SSC, 50% formamide	67°C; 0.3×SSC
D	DNA : RNA	<50	T _D *; 1×SSC	T _D *; 1×SSC
E	RNA : RNA	≥50	70°C; 1×SSC -or- 50°C; 1×SSC, 50% formamide	70°C; 0.3×SSC
F	RNA : RNA	<50	T _F *; 1×SSC	T _F *; 1×SSC
G	DNA : DNA	≥50	65°C; 4×SSC -or- 42°C; 4×SSC, 50% formamide	65°C; 1×SSC
H	DNA : DNA	<50	T _H *; 4×SSC	T _H *; 4×SSC
I	DNA : RNA	≥50	67°C; 4×SSC -or- 45°C; 4×SSC, 50% formamide	67°C; 1×SSC
J	DNA : RNA	<50	T _J *; 4×SSC	T _J *; 4×SSC
K	RNA : RNA	≥50	70°C; 4×SSC -or- 50°C; 4×SSC, 50% formamide	67°C; 1×SSC
L	RNA : RNA	<50	T _L *; 2×SSC	T _L *; 2×SSC
M	DNA : DNA	≥50	50°C; 4×SSC -or- 40°C; 6×SSC, 50% formamide	50°C; 2×SSC
N	DNA : DNA	<50	T _N *; 6×SSC	T _N *; 6×SSC
O	DNA : RNA	≥50	55°C; 4×SSC -or- 42°C; 6×SSC, 50% formamide	55°C; 2×SSC
P	DNA : RNA	<50	T _P *; 6×SSC	T _P *; 6×SSC
Q	RNA : RNA	≥50	60°C; 4×SSC -or- 45°C; 6×SSC, 50% formamide	60°C; 2×SSC
R	RNA : RNA	<50	T _R *; 4×SSC	T _R *; 4×SSC

‡ : The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

† : SSPE (1×SSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH7.4) can be substituted for SSC (1×SSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R : The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C)=2(#of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C)=81.5 + 16.6(log₁₀[Na⁺]) + 0.41 (%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1×SSC=0.165M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and Current Protocols in Molecular Biology, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

10 Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more
15 preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and
20 identity while minimizing sequence gaps.

CLAIMS

1. A protein comprising any one of amino acid sequences selected from the group consisting of SEQ ID NOS:
5 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130.
2. An isolated DNA encoding the protein according to Claim 1.
3. An isolated cDNA comprising any one of base sequences selected from the group consisting of SEQ ID NOS:
10 11 to 20, 41 to 50, 71 to 80, 101 to 110 and 131 to 140.
4. The cDNA according to Claim 3 consisting of any one of base sequences selected from the group consisting of SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141 to 150.
- 15 5. An expression vector that is capable of expressing the DNA according to any one of Claim 2 to Claim 4 by in vitro translation or in eukaryotic cells.
6. A transformed eukaryotic cell that is capable of expressing the DNA according to any one of Claim 2 to Claim
20 4 and of producing the protein according to Claim 1.
7. An antibody directed to the protein according to Claim 1.

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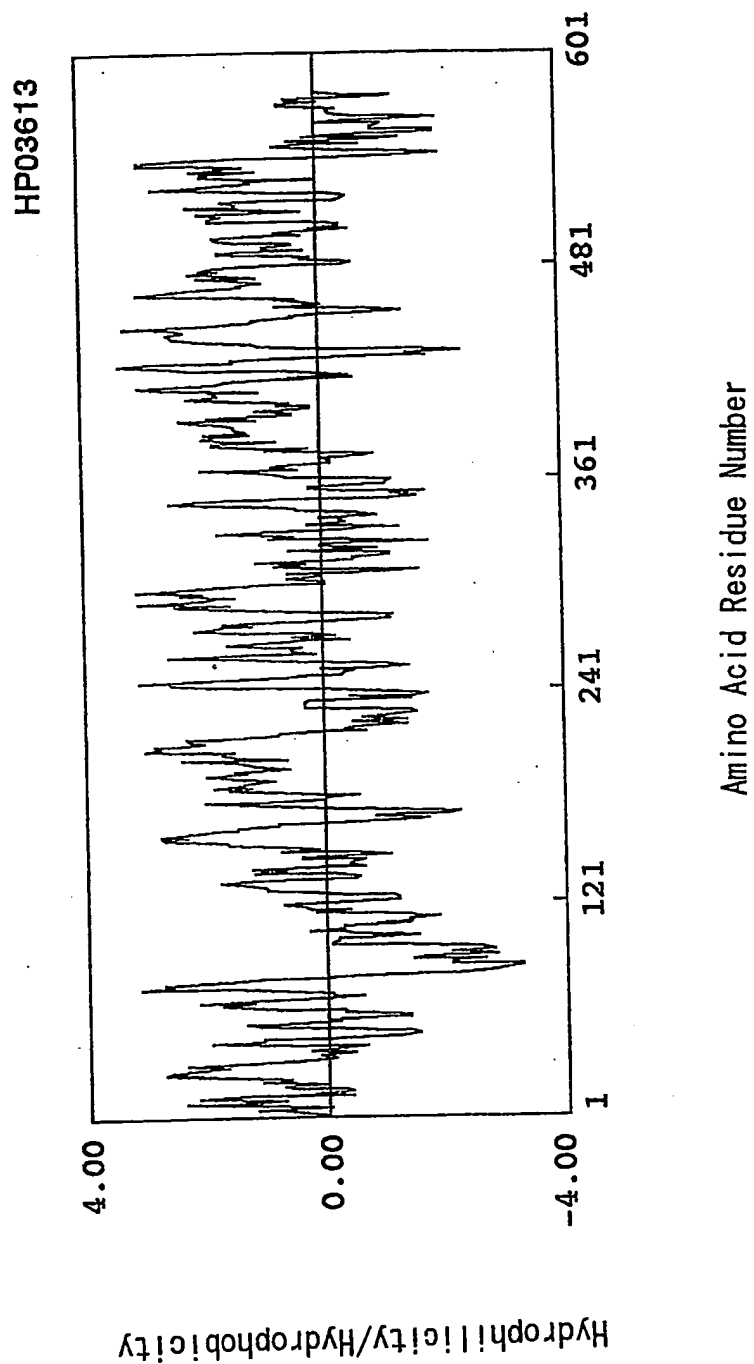


Fig. 1

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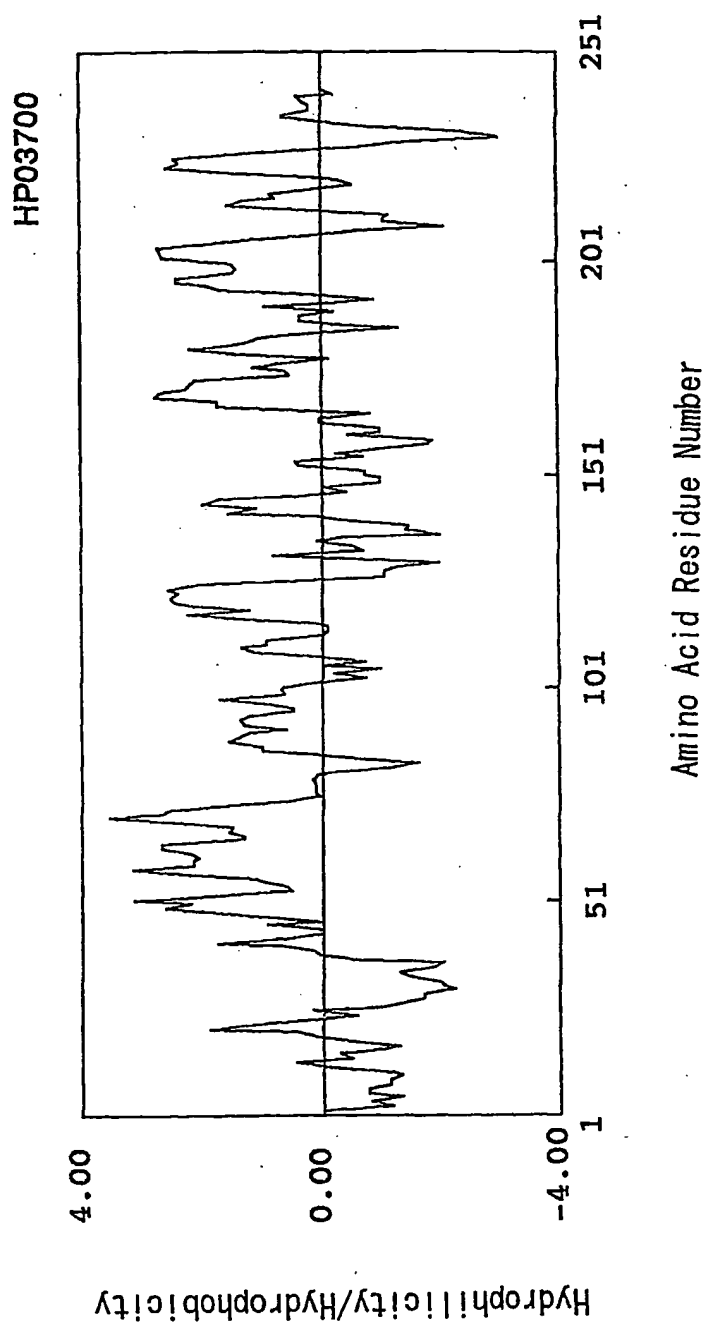


Fig. 2

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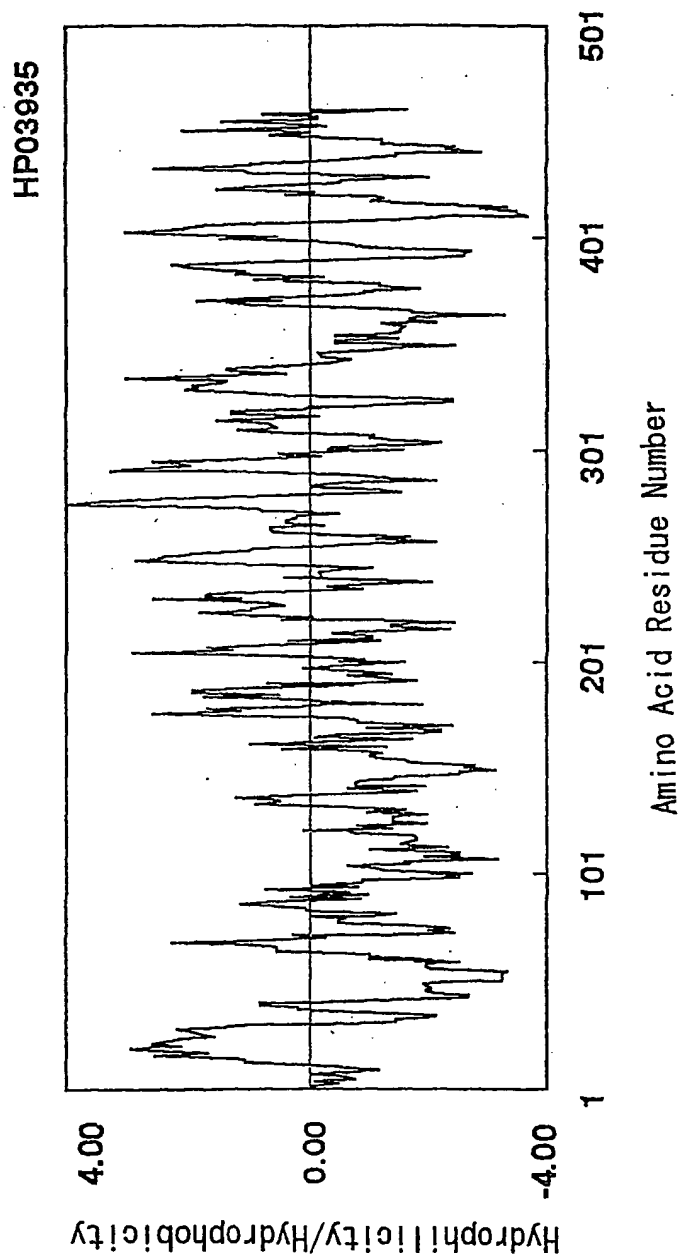


Fig. 3

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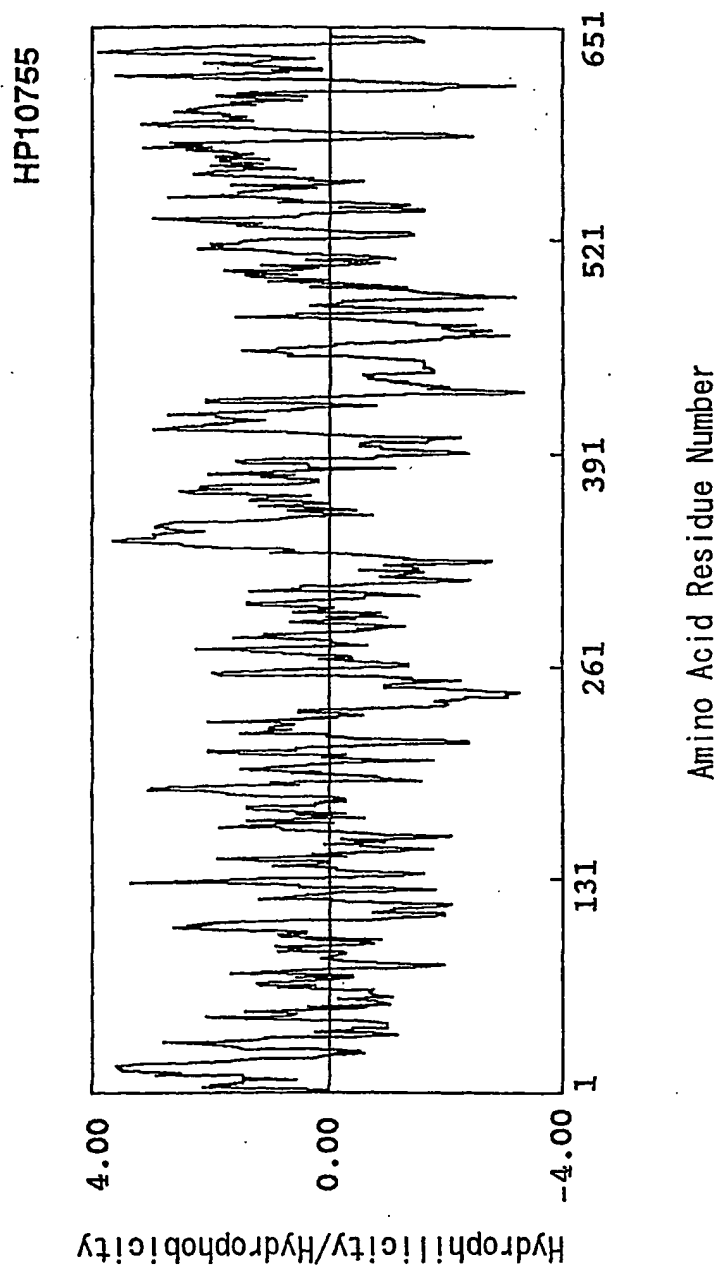


Fig. 4

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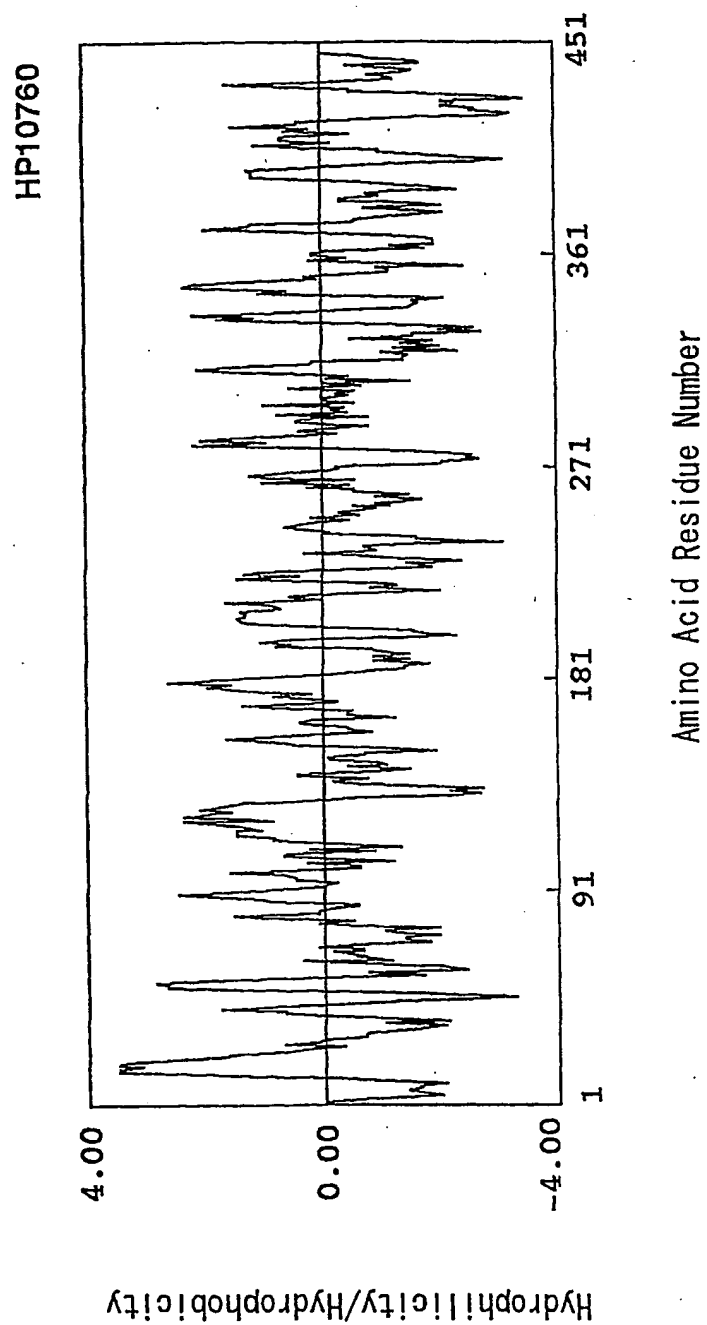


Fig. 5

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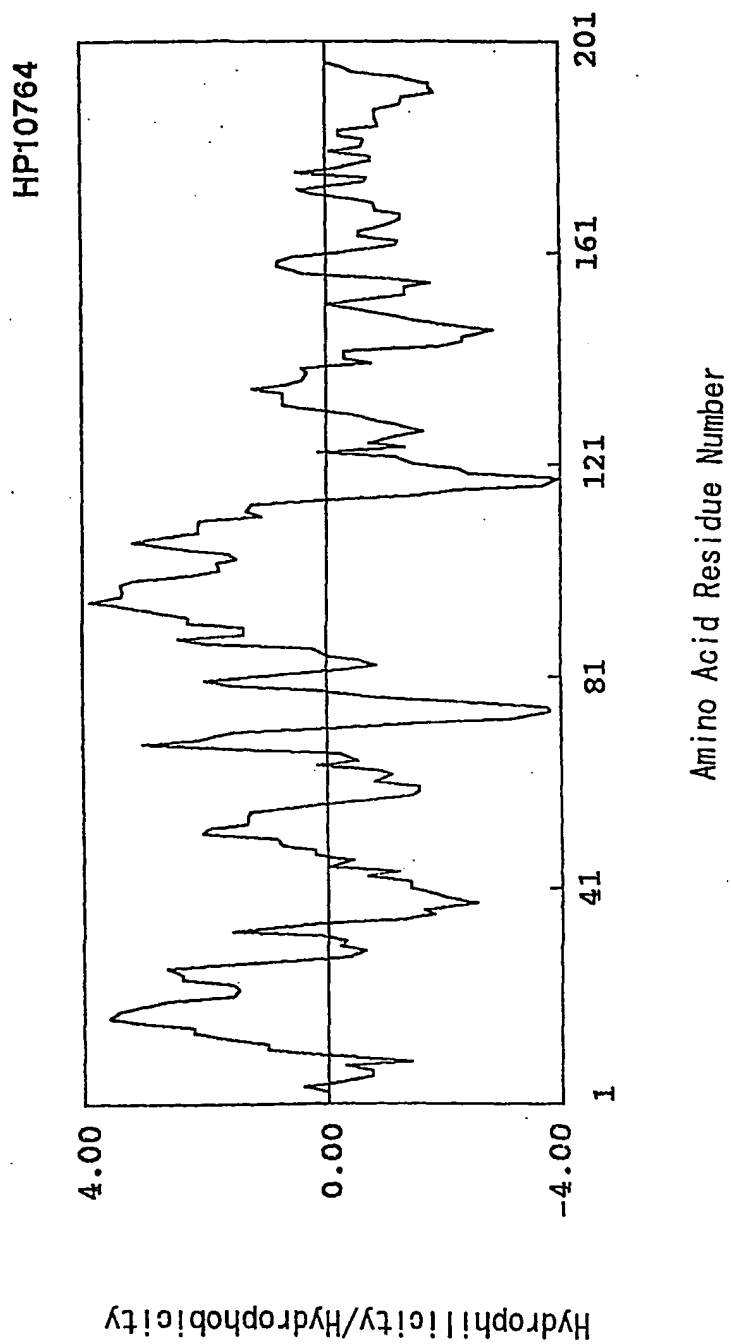


Fig. 6

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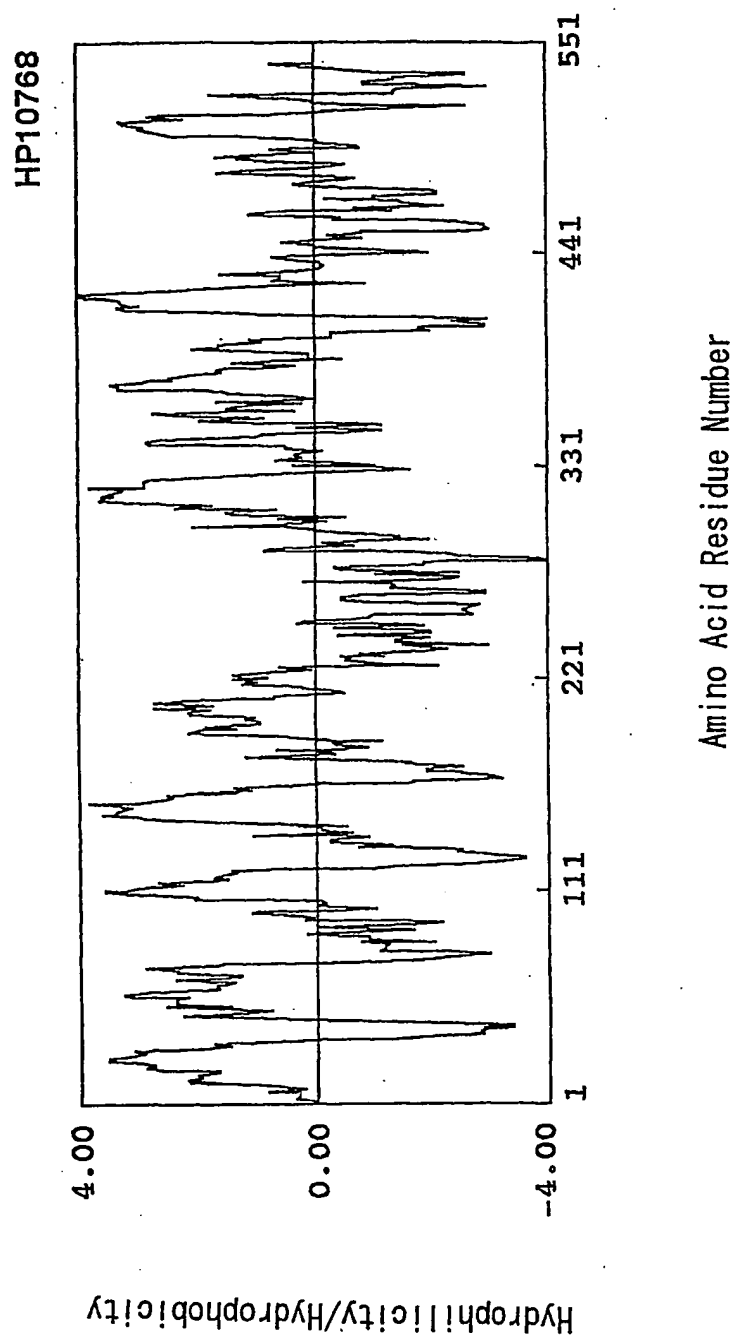


Fig. 7

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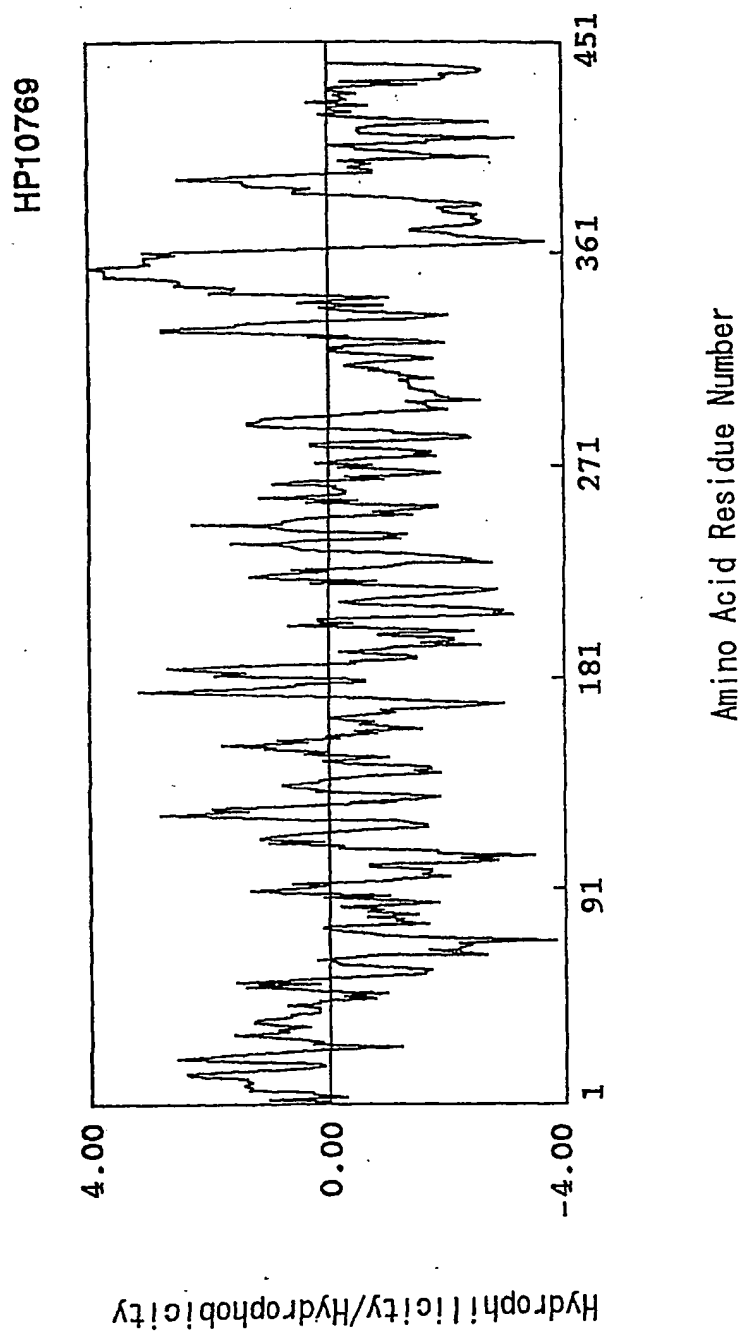


Fig. 8

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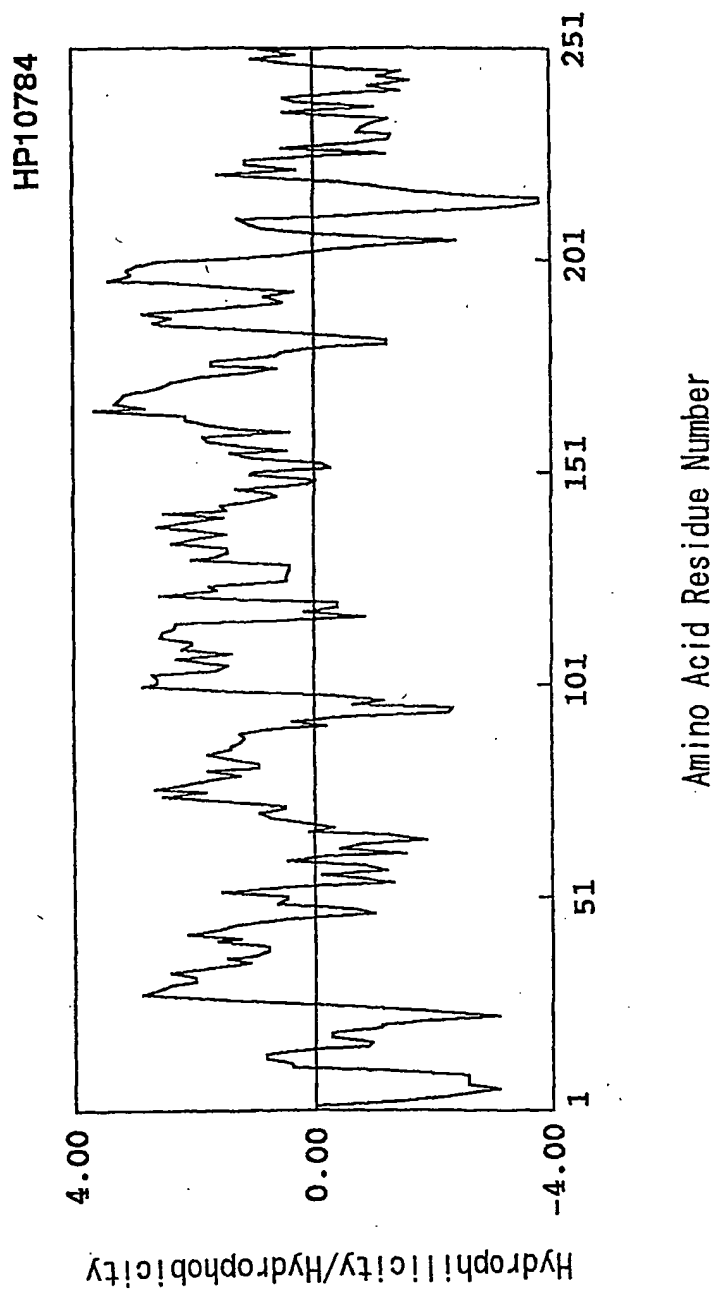


Fig. 9

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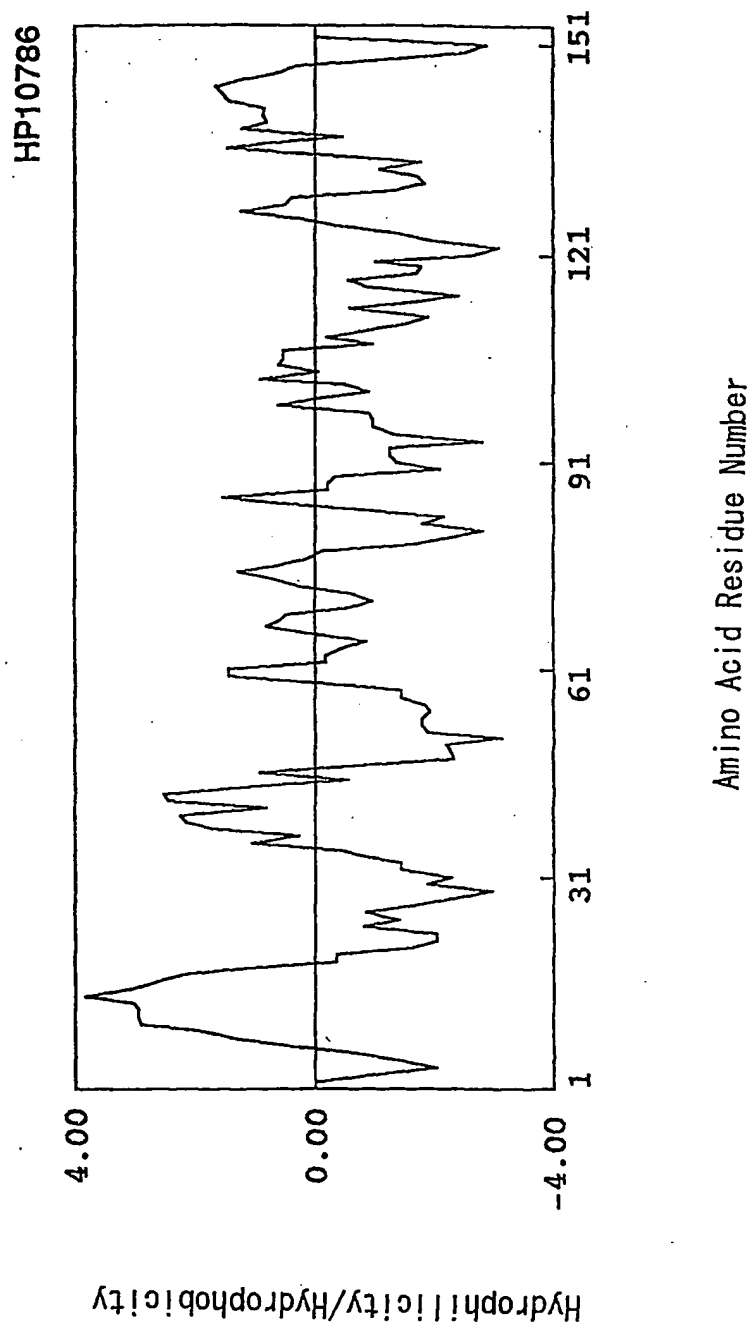


Fig. 10

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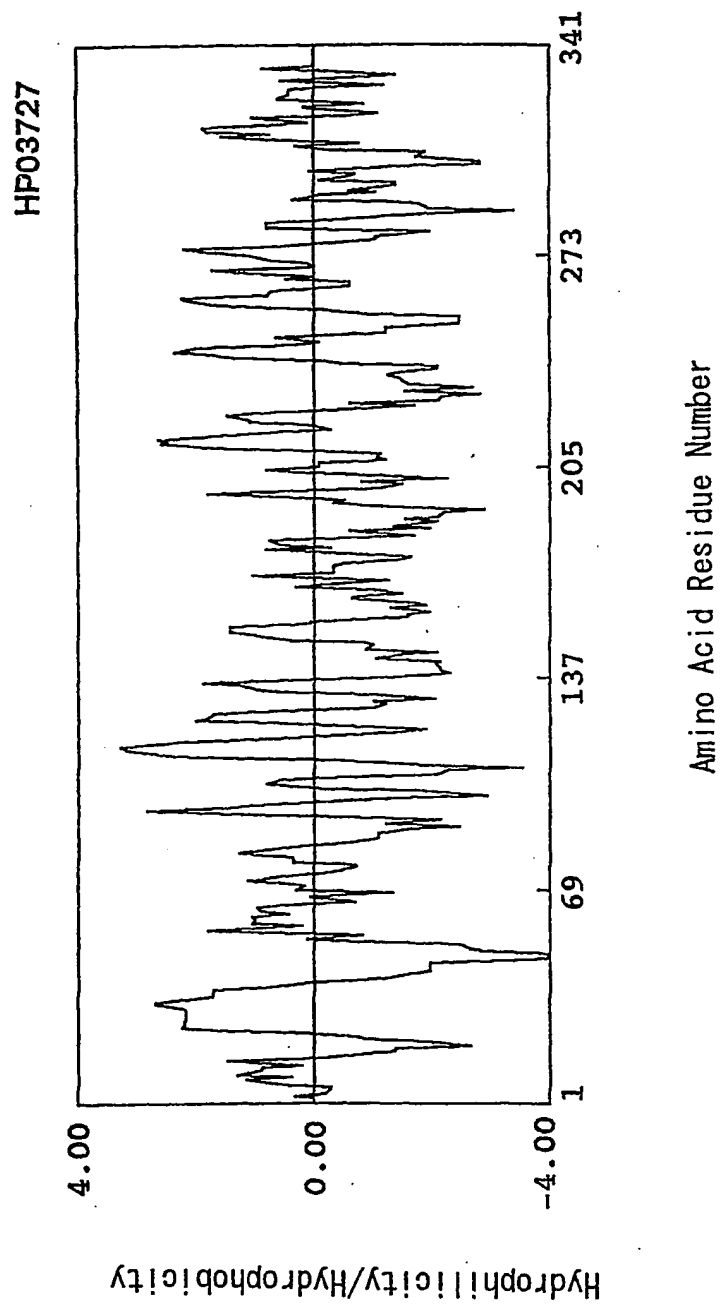


Fig. 11

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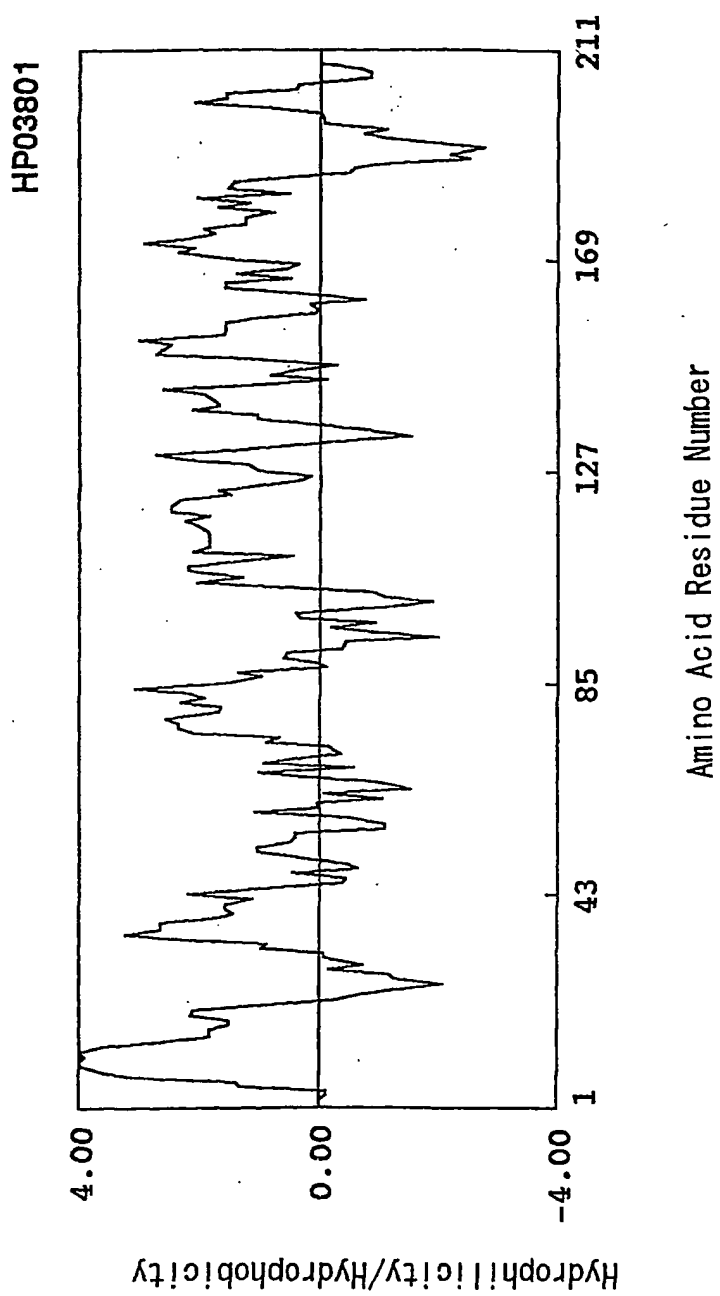


Fig. 12

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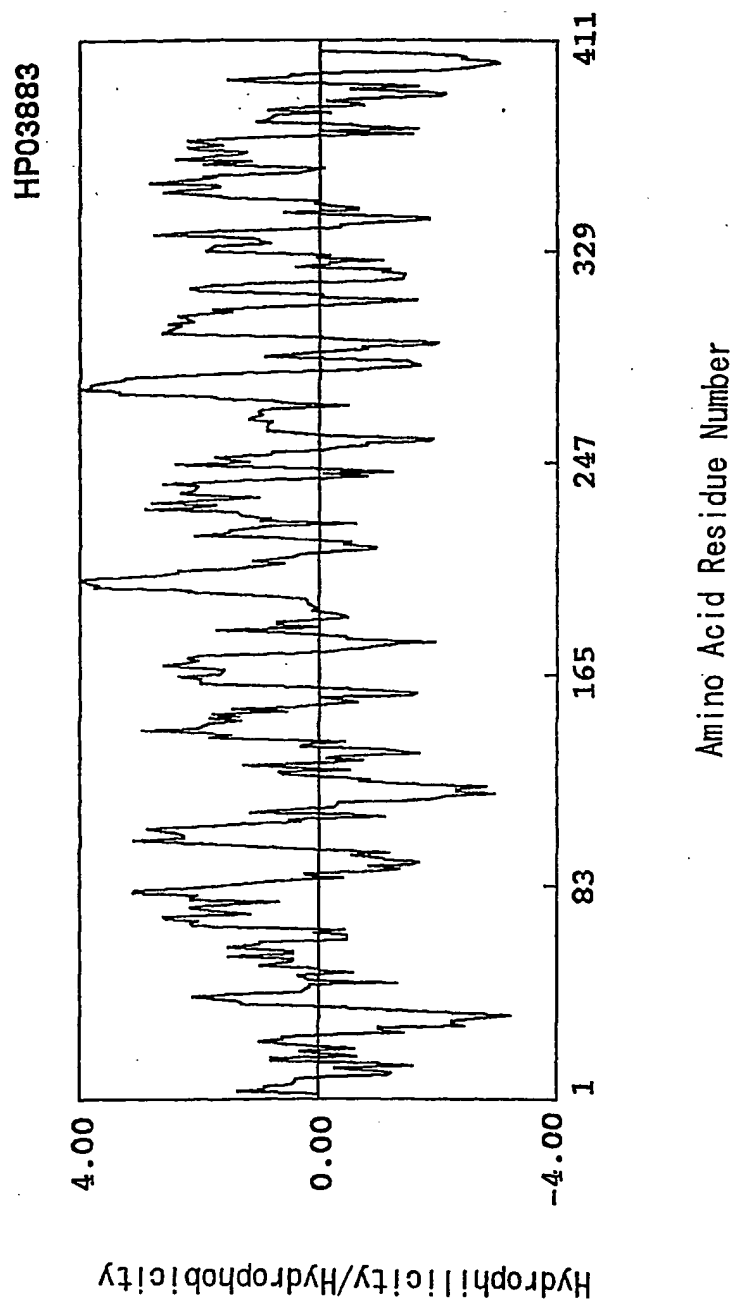


Fig. 13

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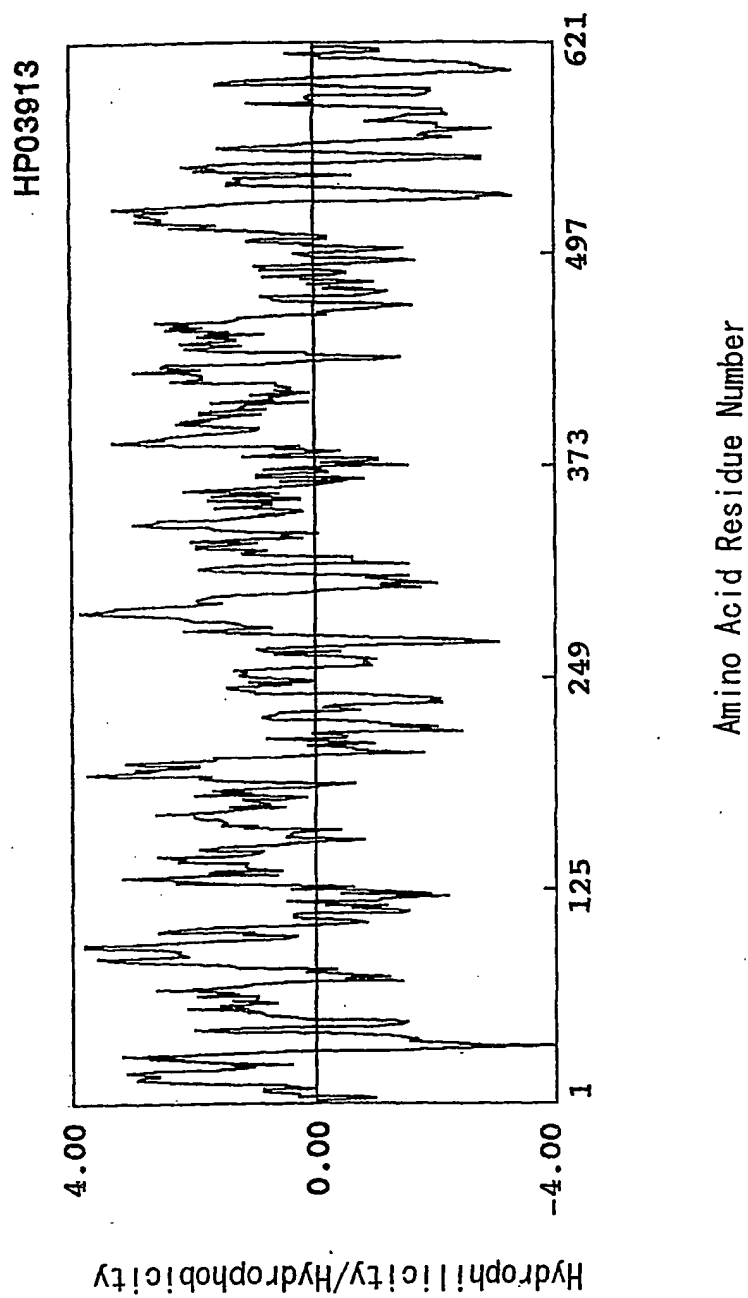


Fig. 14

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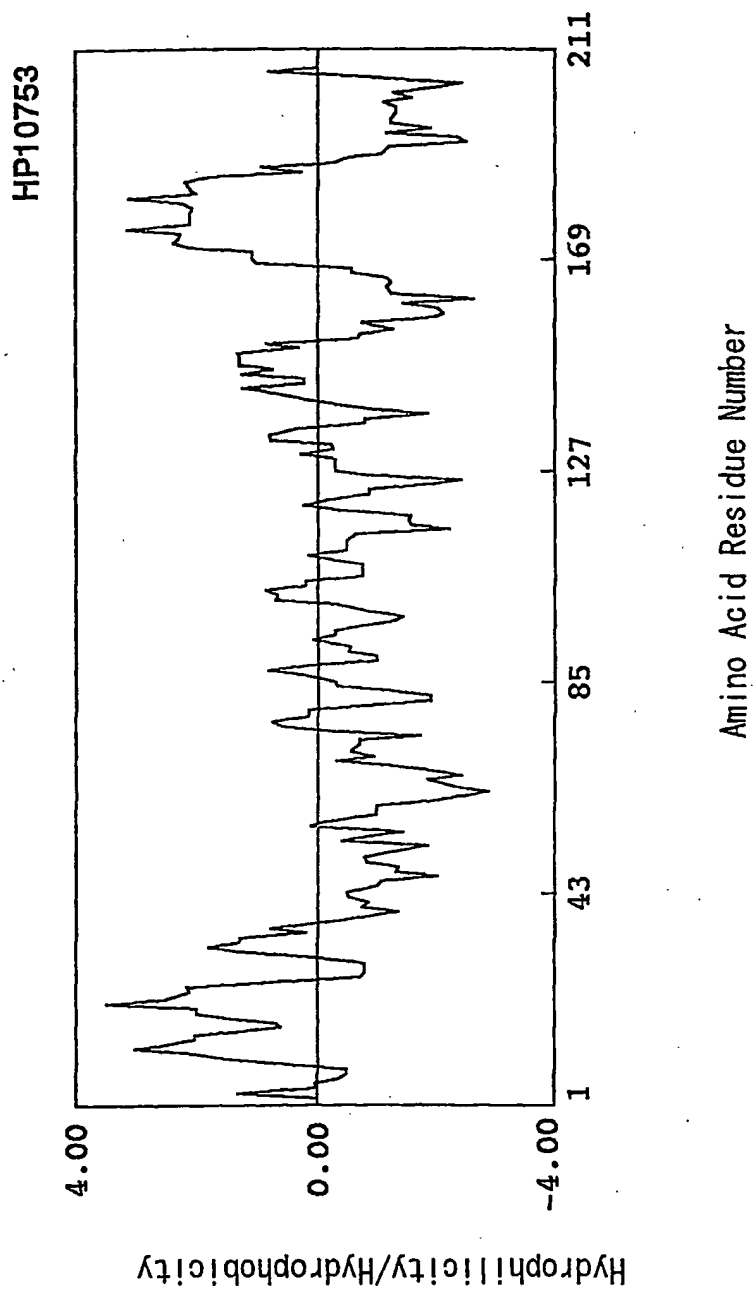


Fig. 15

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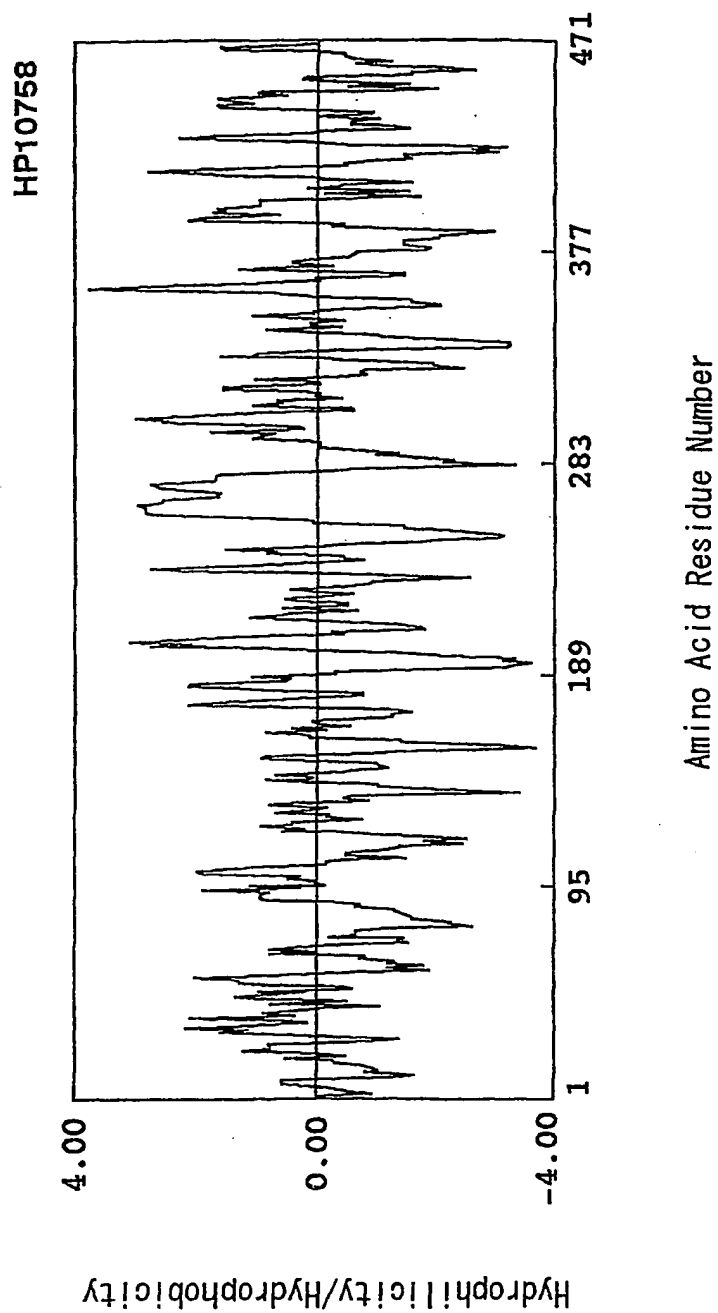


Fig. 16

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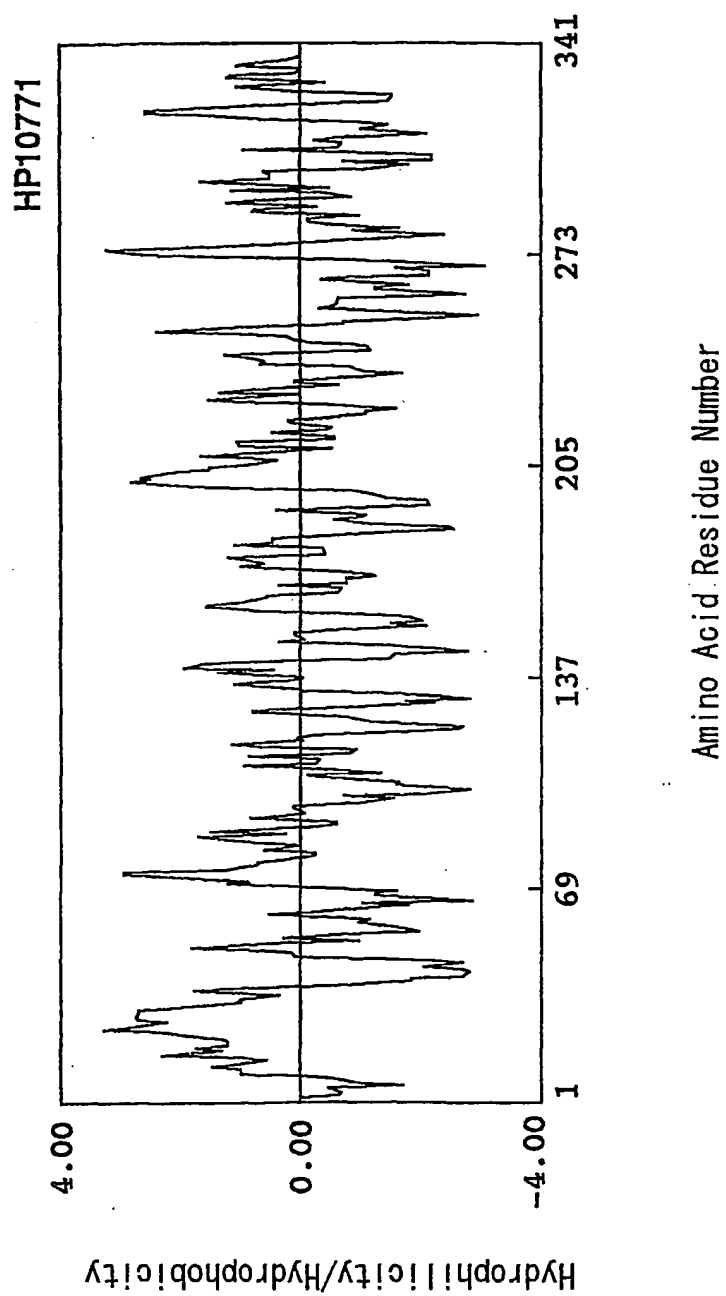


Fig. 17

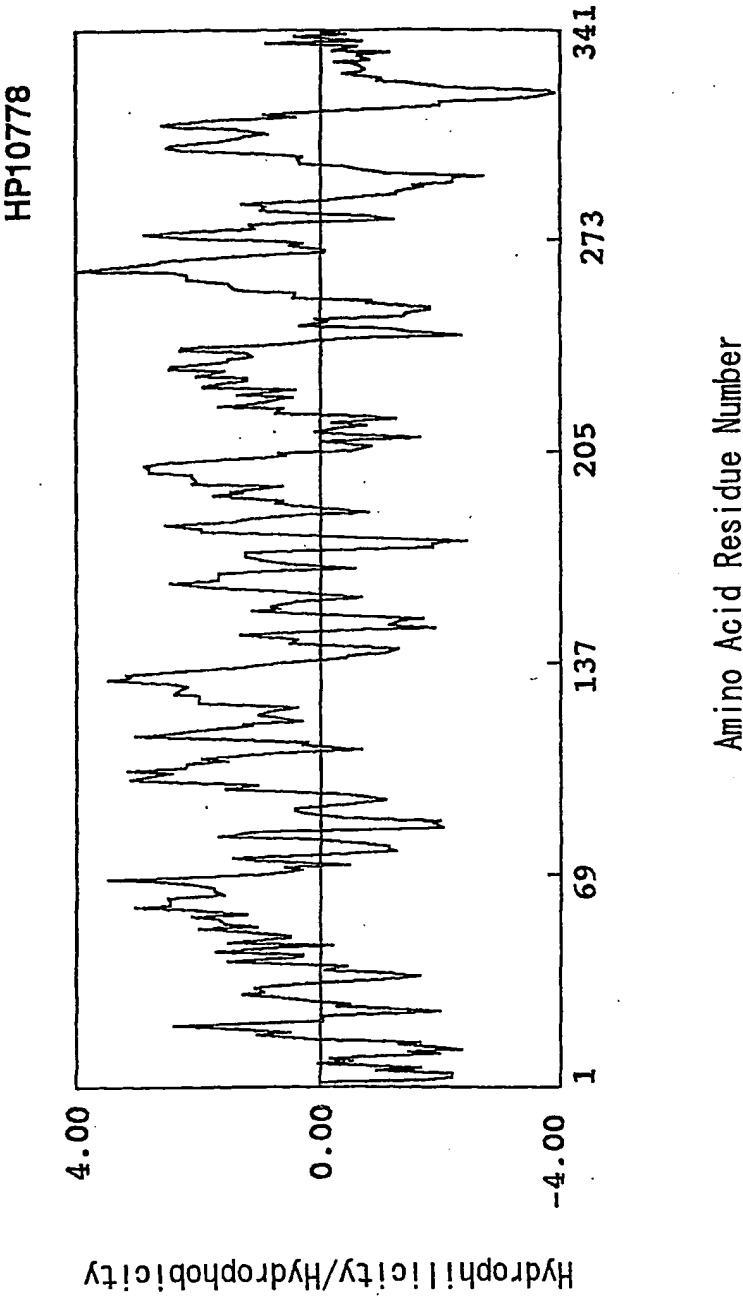


Fig. 18

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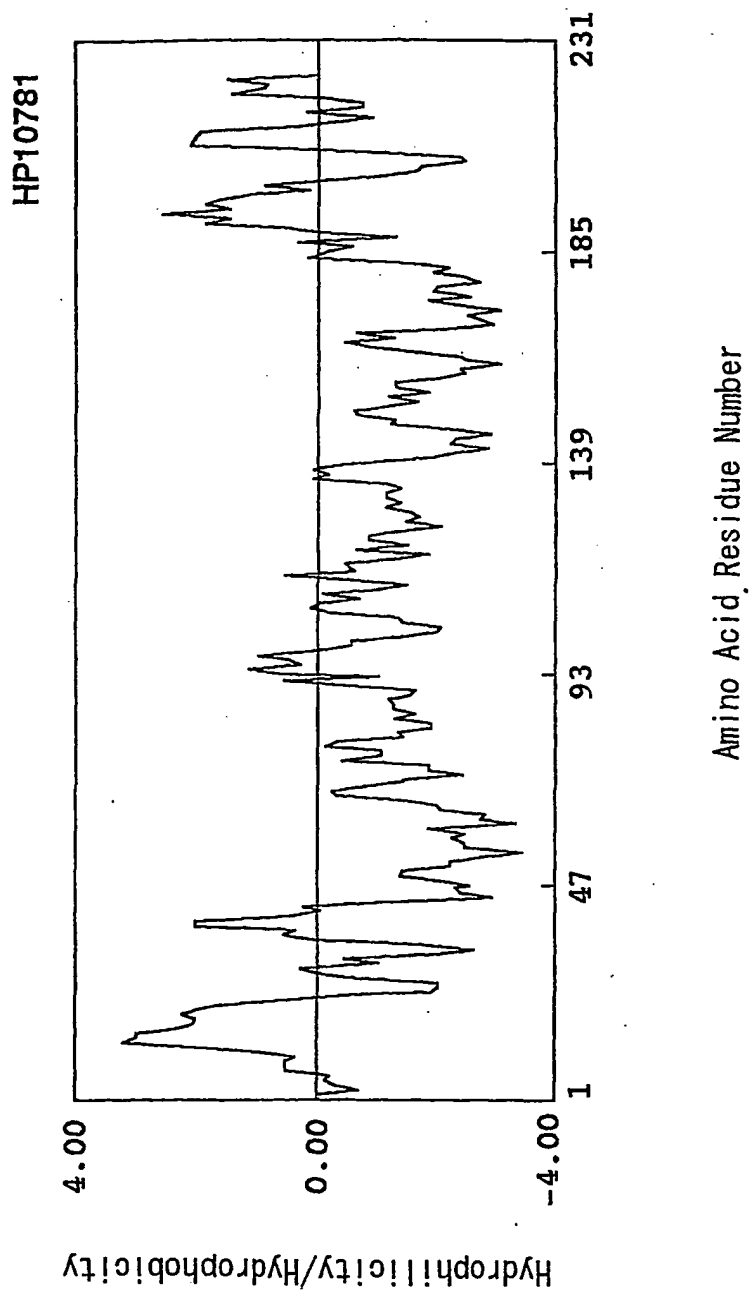


Fig. 19

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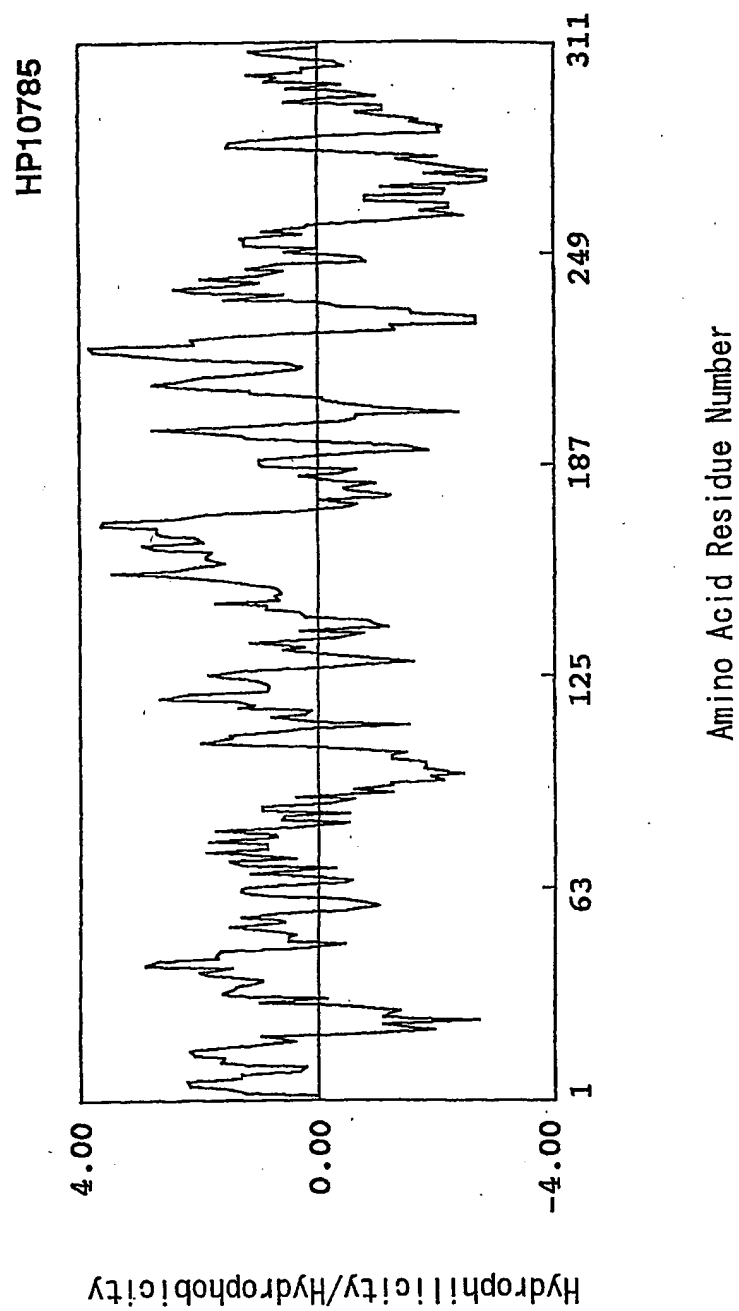


Fig. 20

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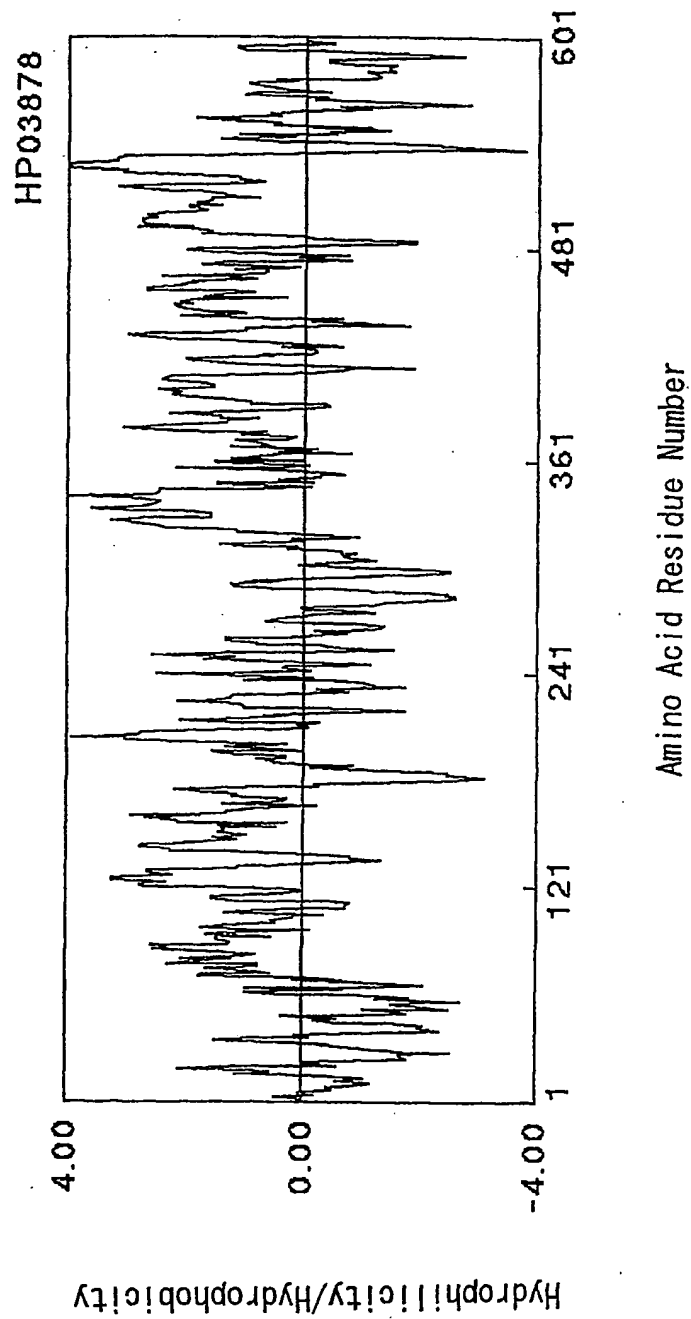


Fig. 21

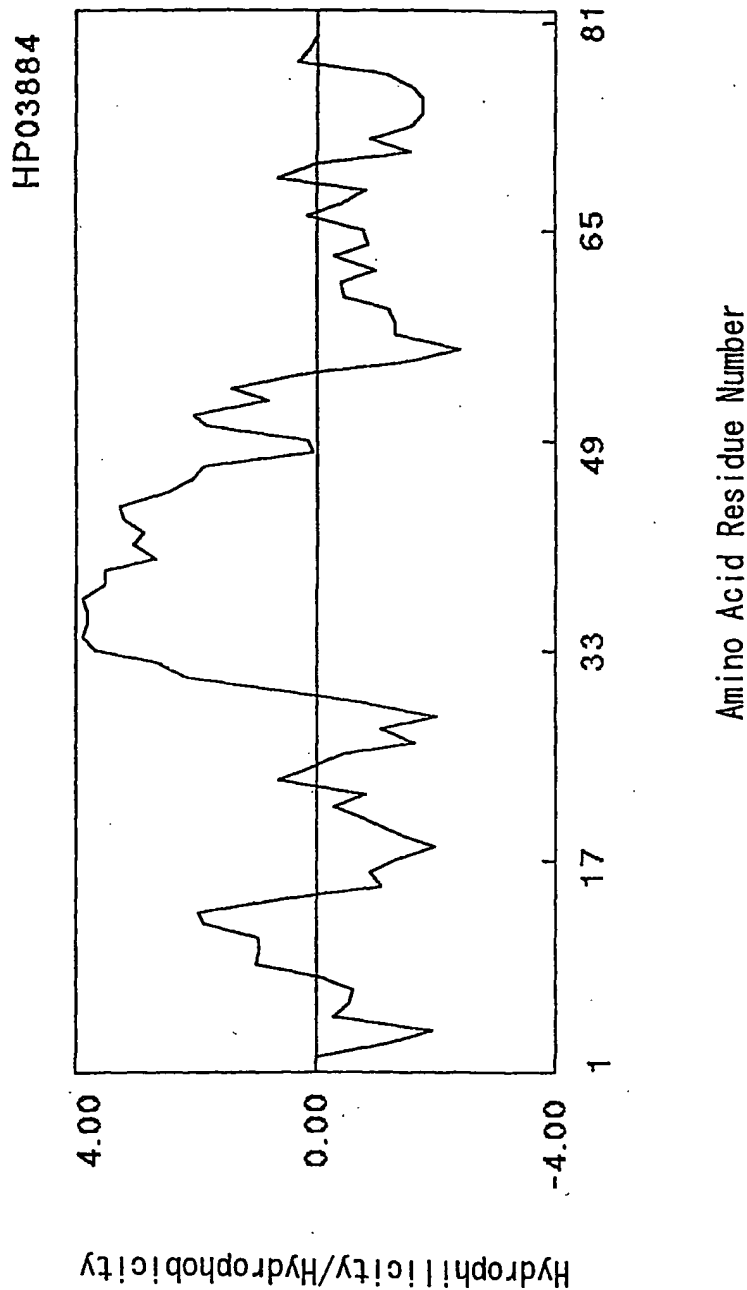


Fig. 22

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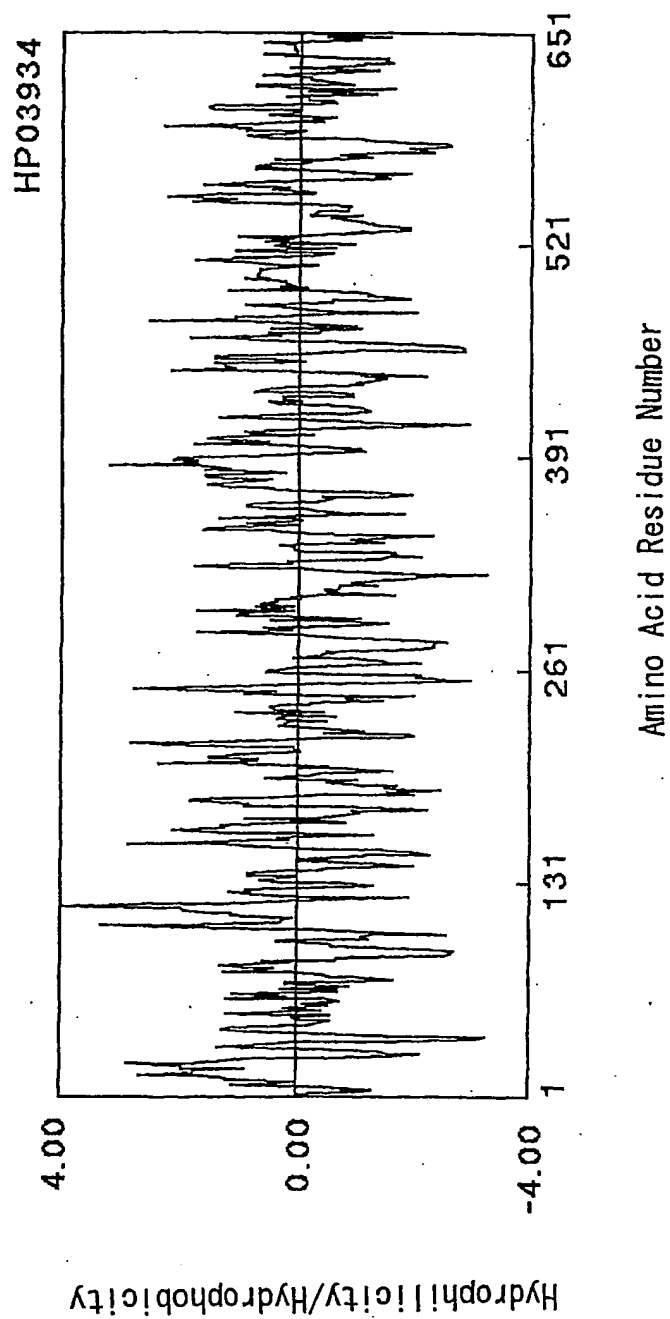


Fig. 23

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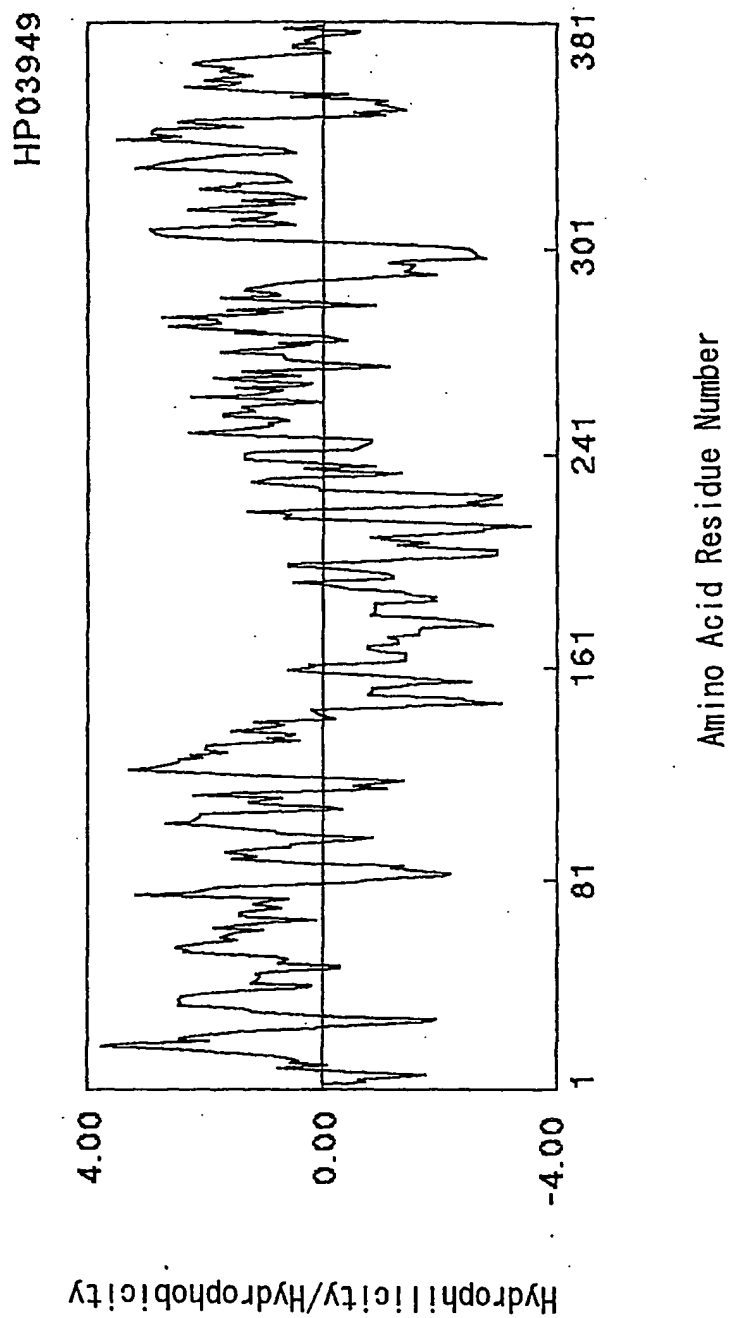


Fig. 24

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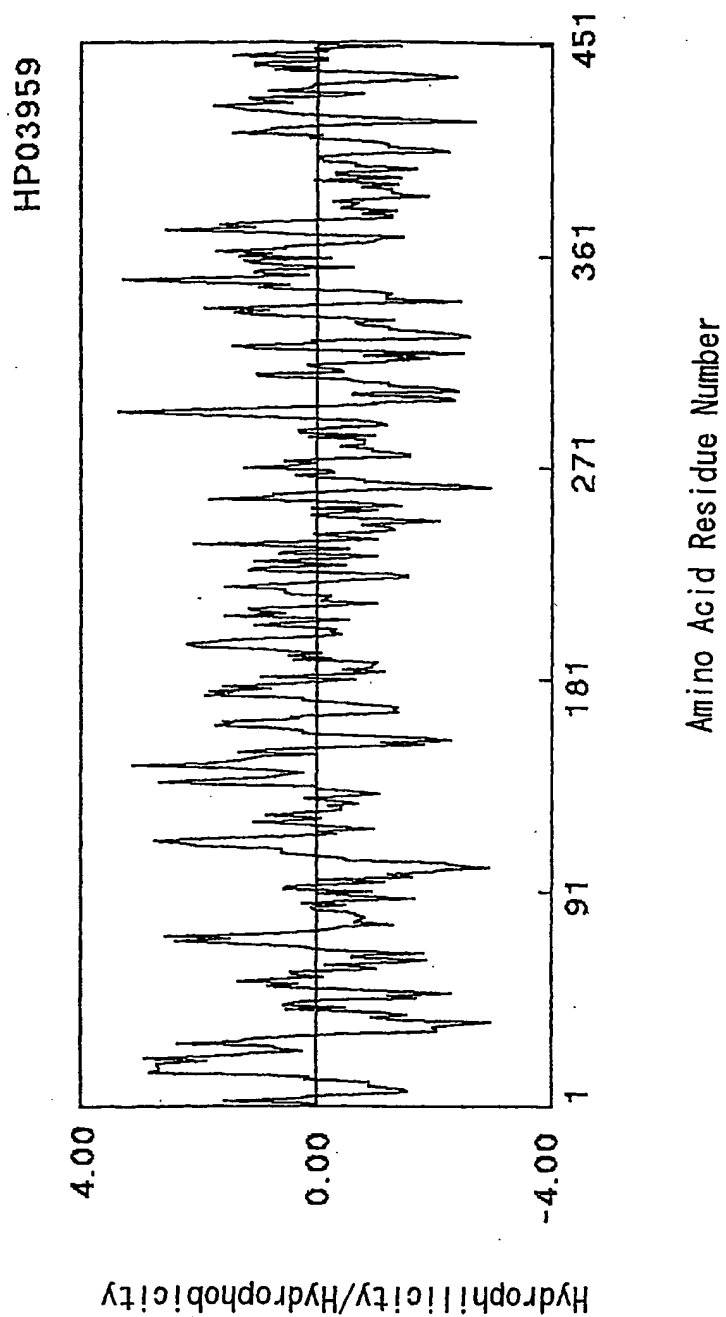


Fig. 25

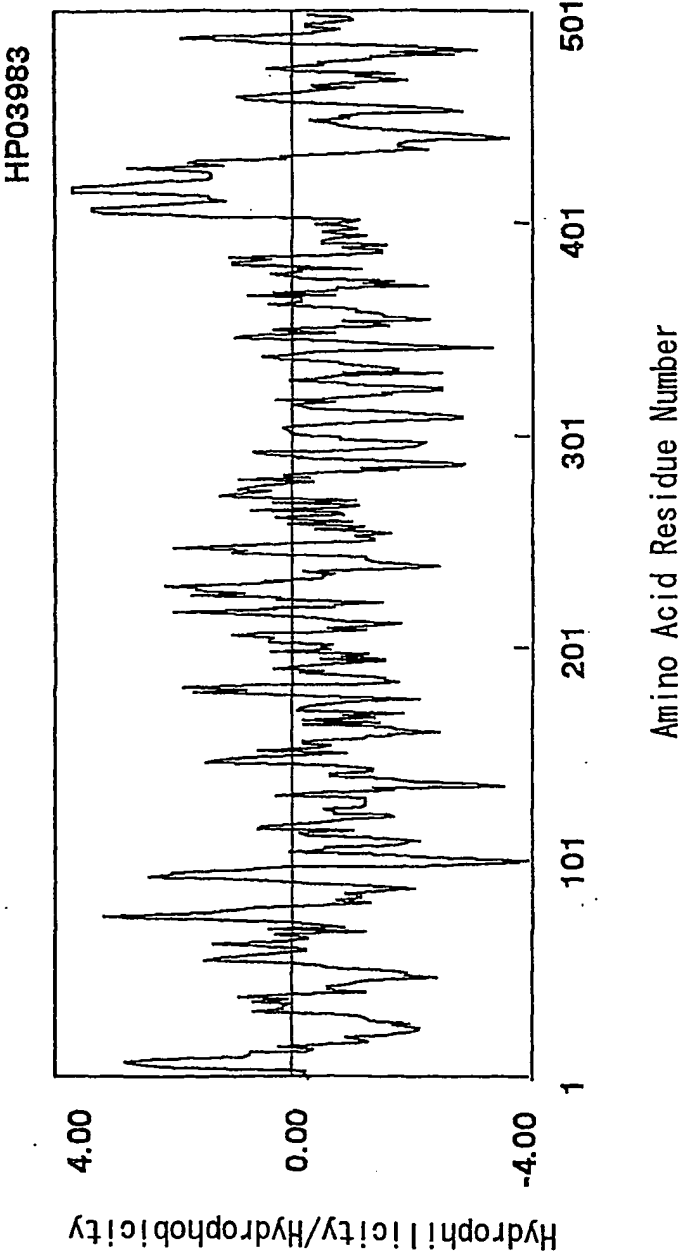


Fig. 26

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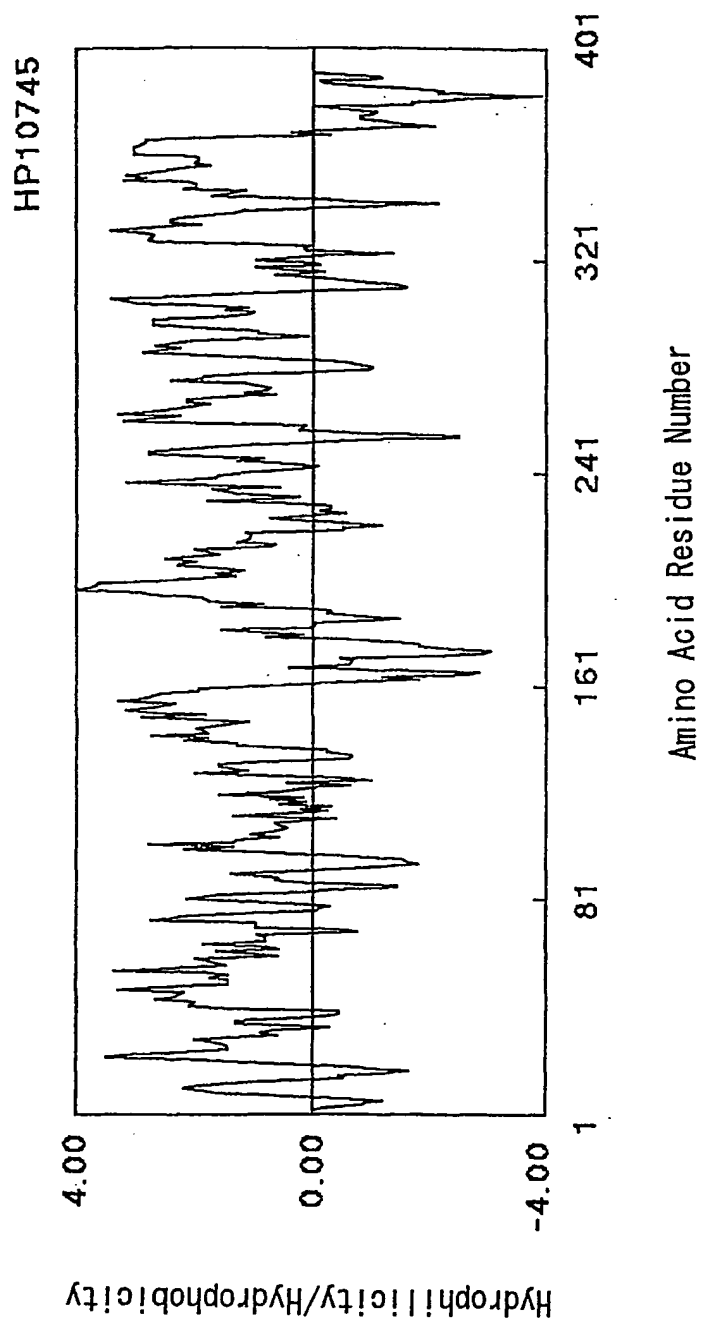


Fig. 27

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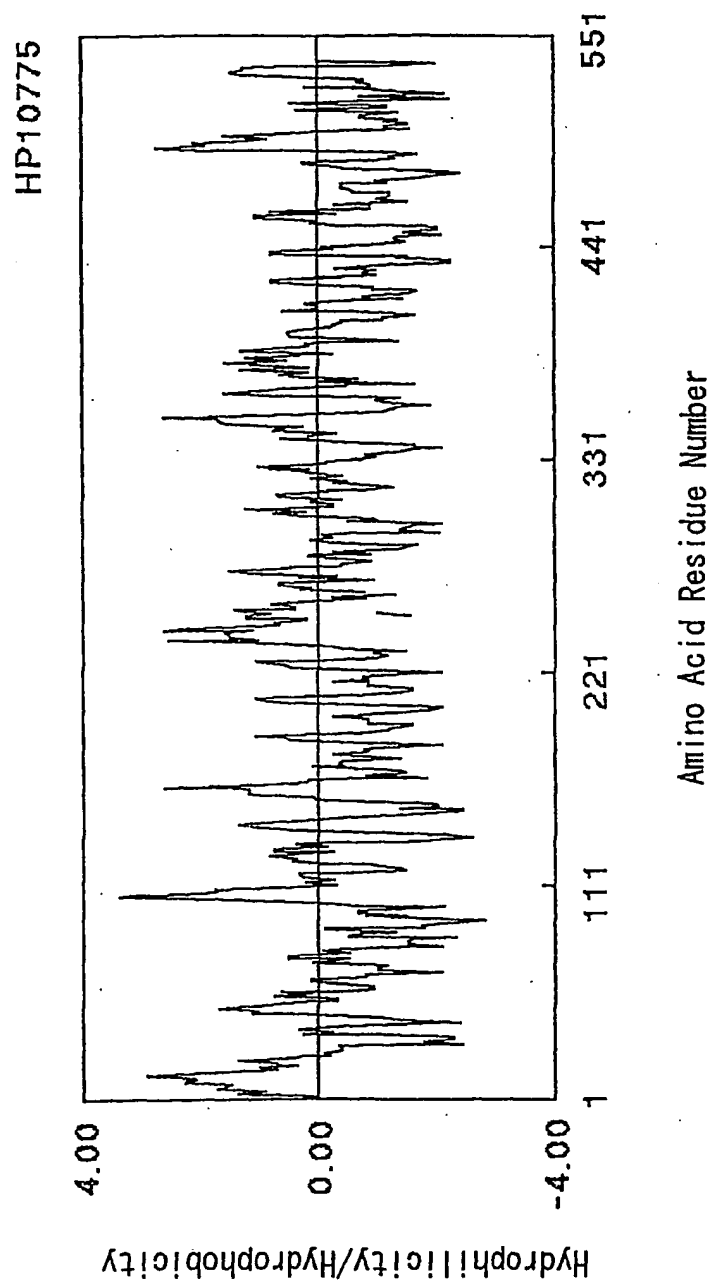


Fig. 28

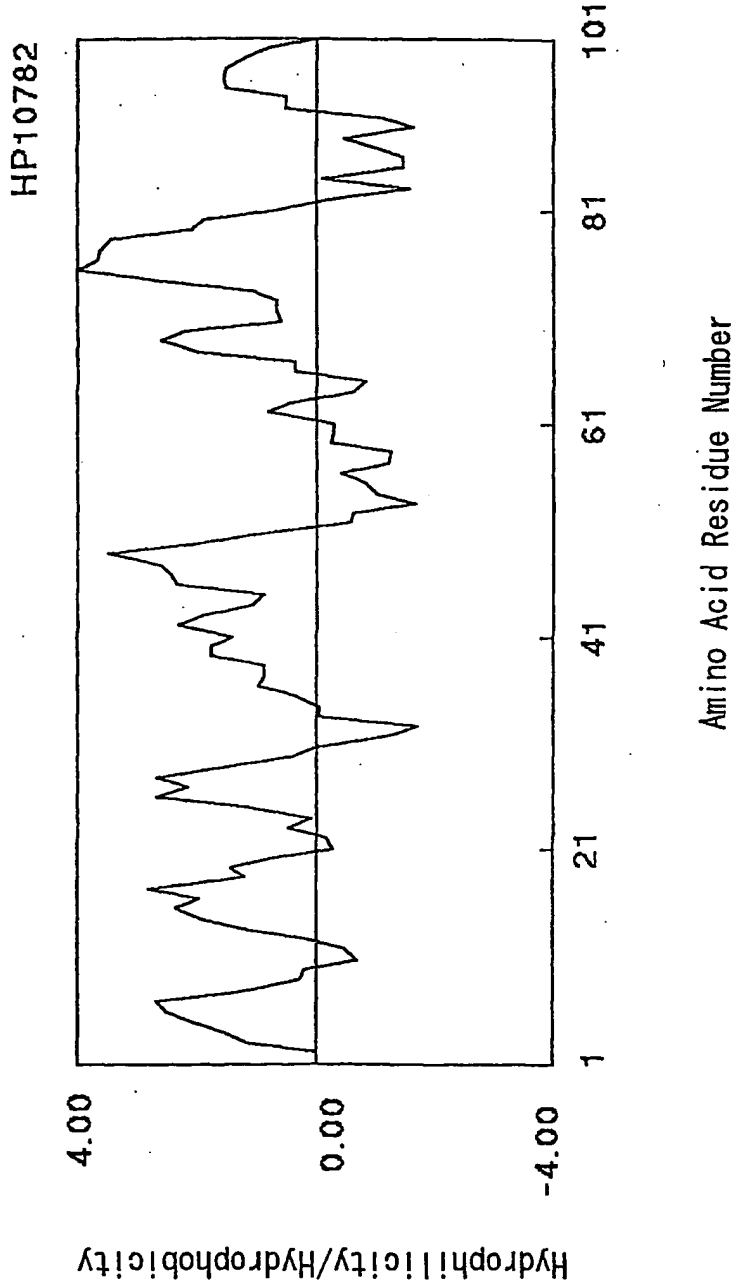


Fig. 29

30/50

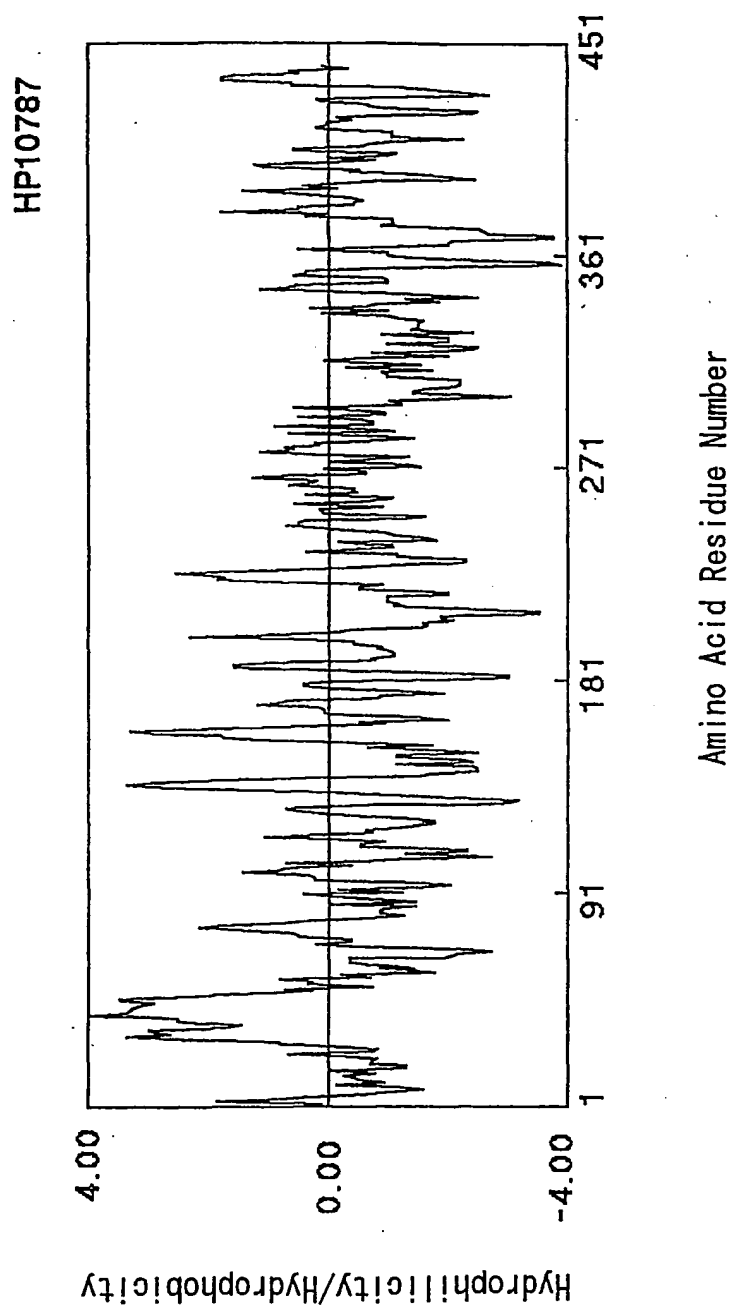
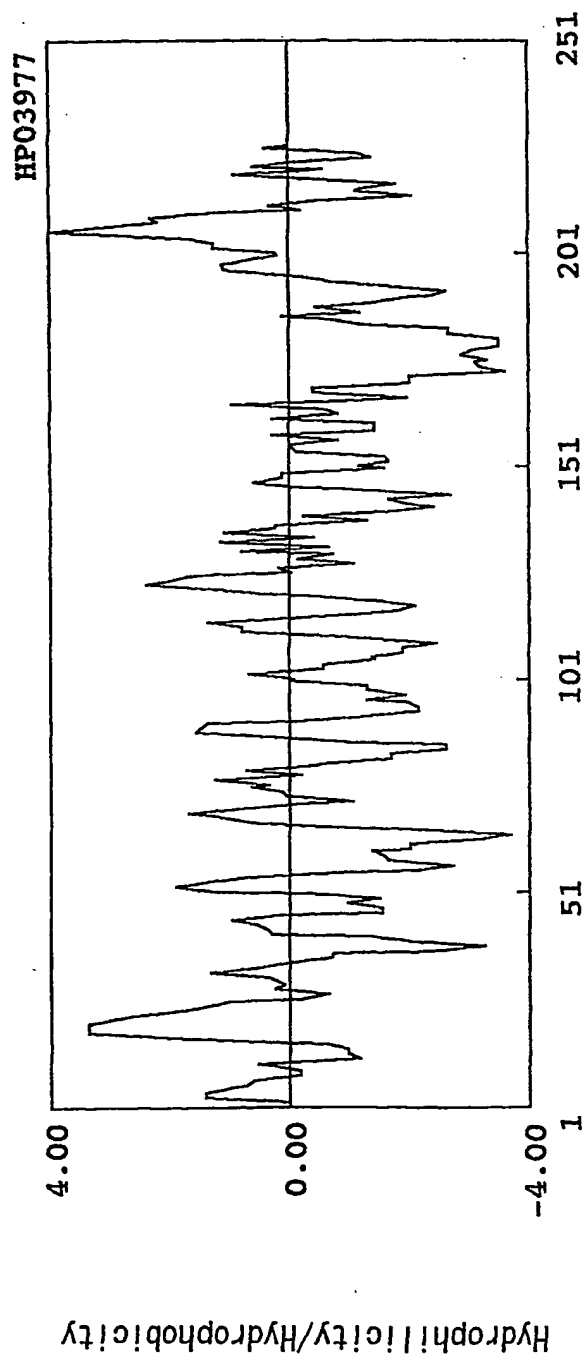


Fig. 30

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Amino Acid Residue Number

Fig. 31

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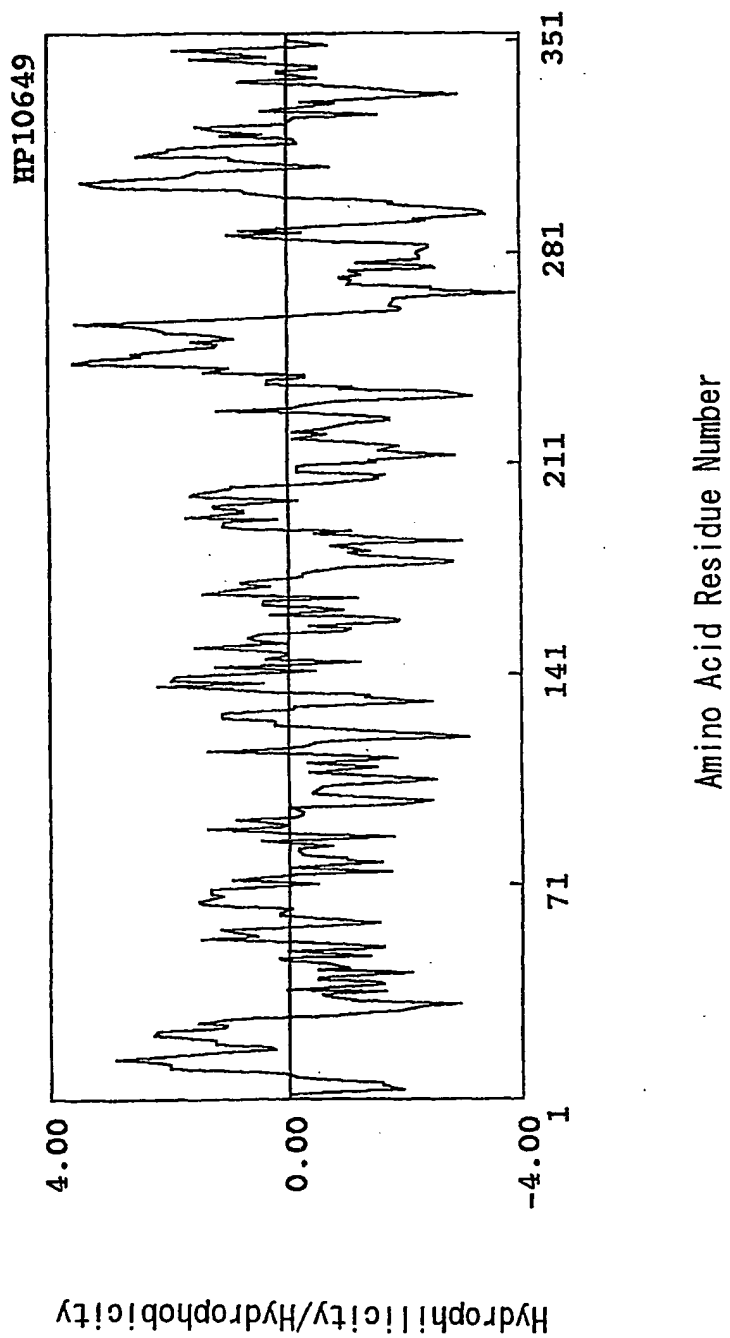
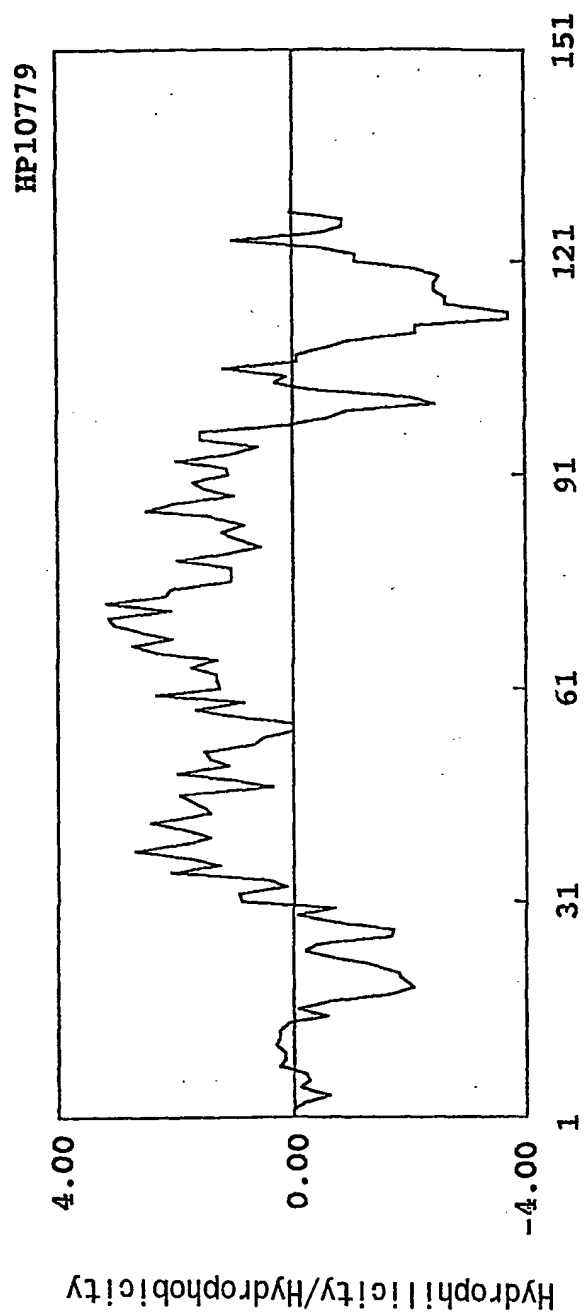


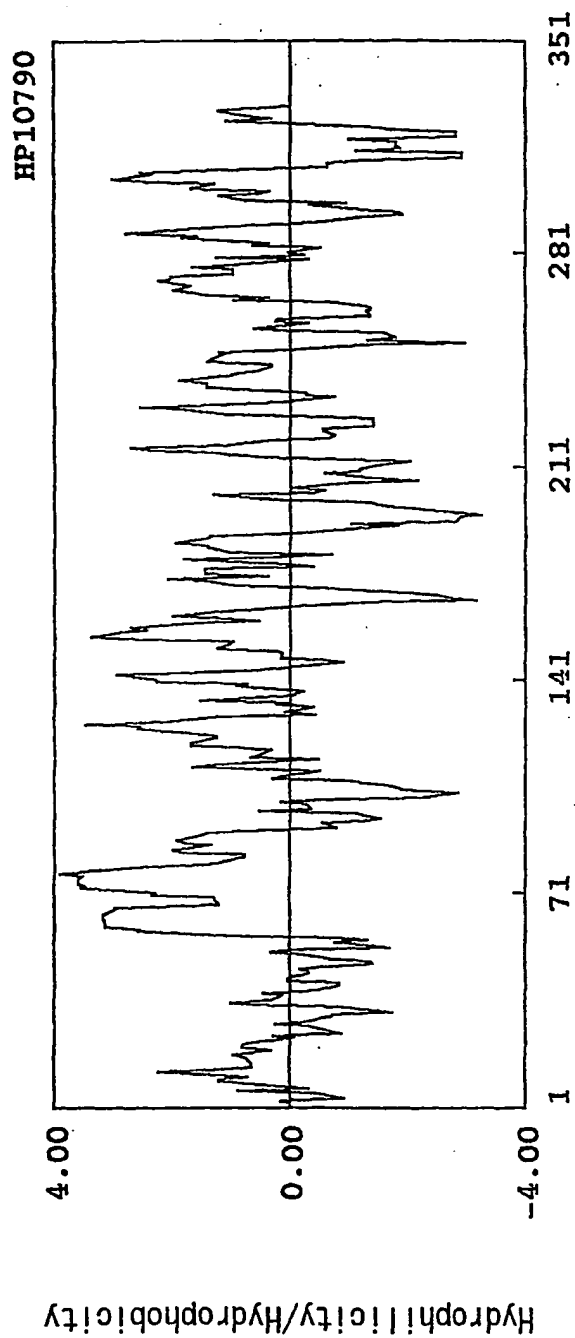
Fig. 32

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Amino Acid Residue Number

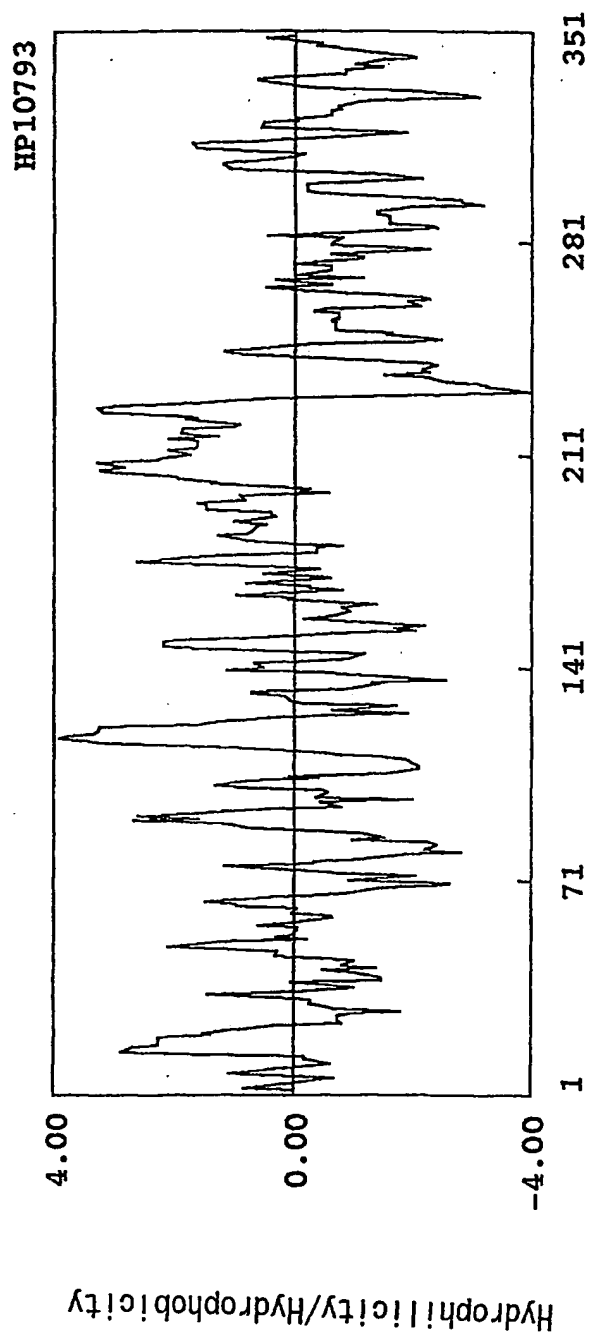
Fig. 33



Amino Acid Residue Number

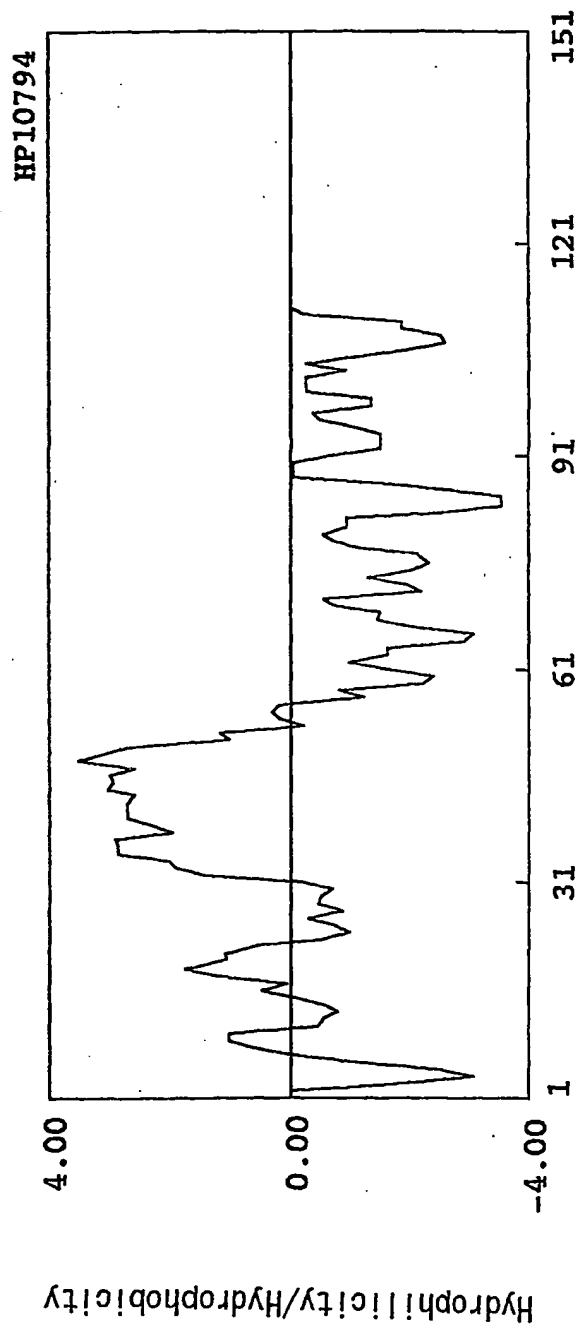
Fig. 34

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Amino Acid Residue Number

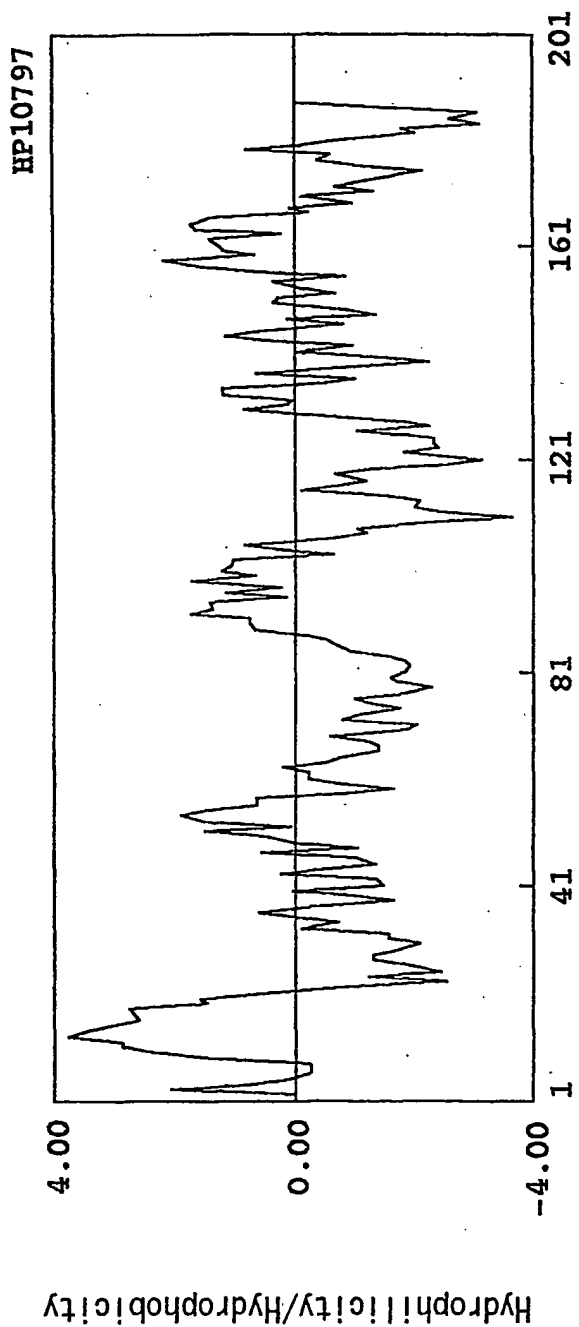
Fig. 35



Amino Acid Residue Number

Fig. 36

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Amino Acid Residue Number

Fig. 37

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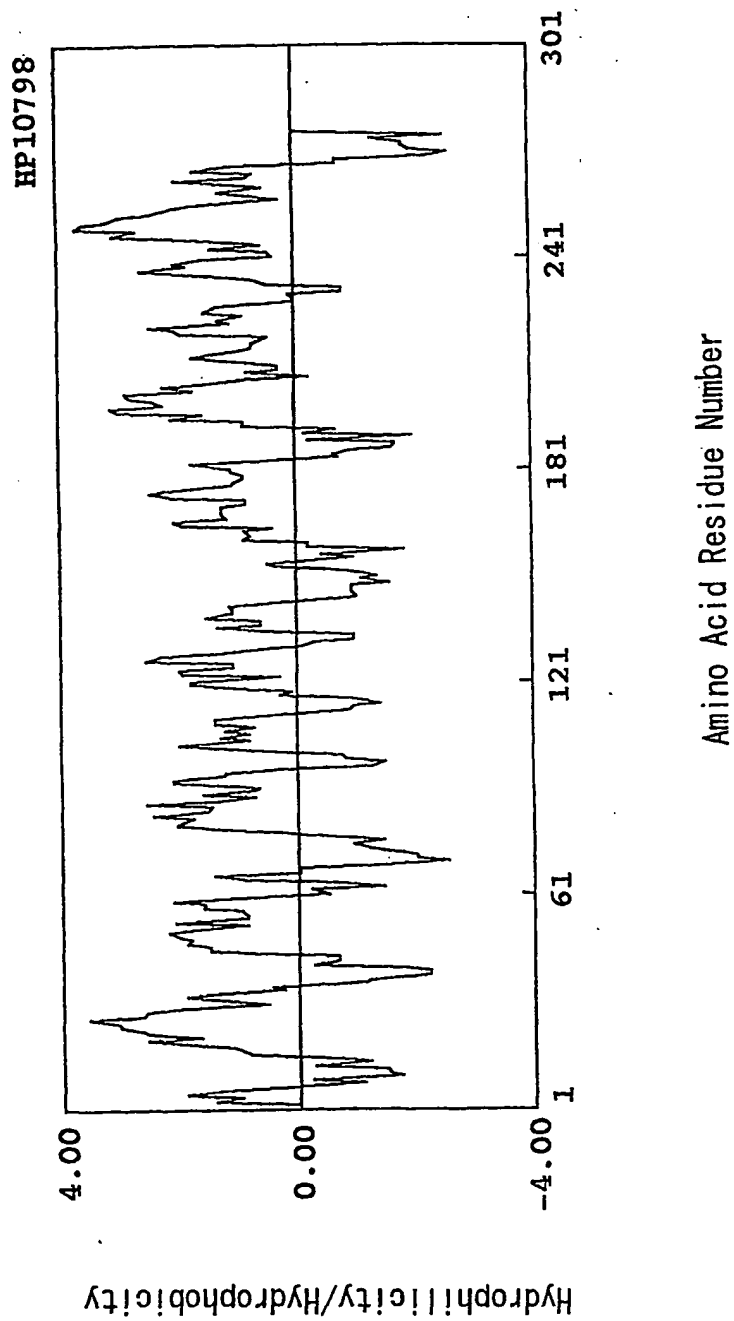


Fig. 38

39/50

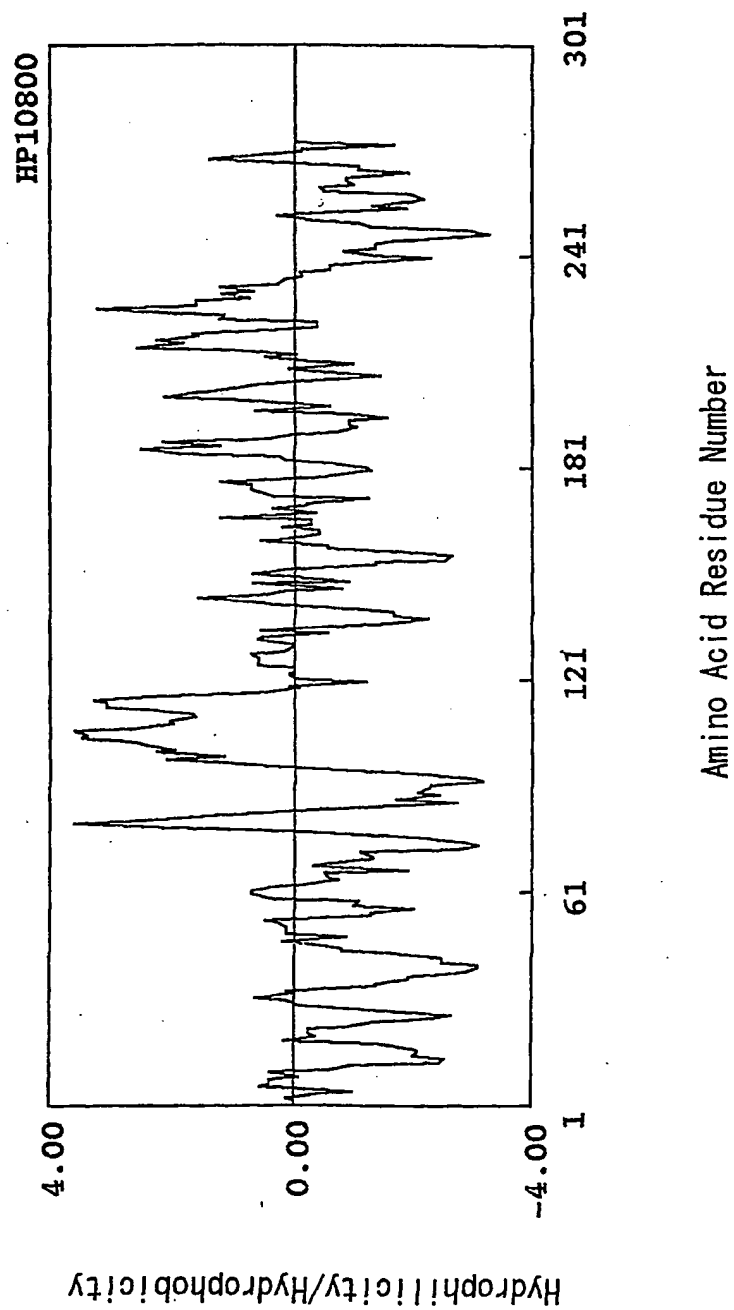


Fig. 39

40/50

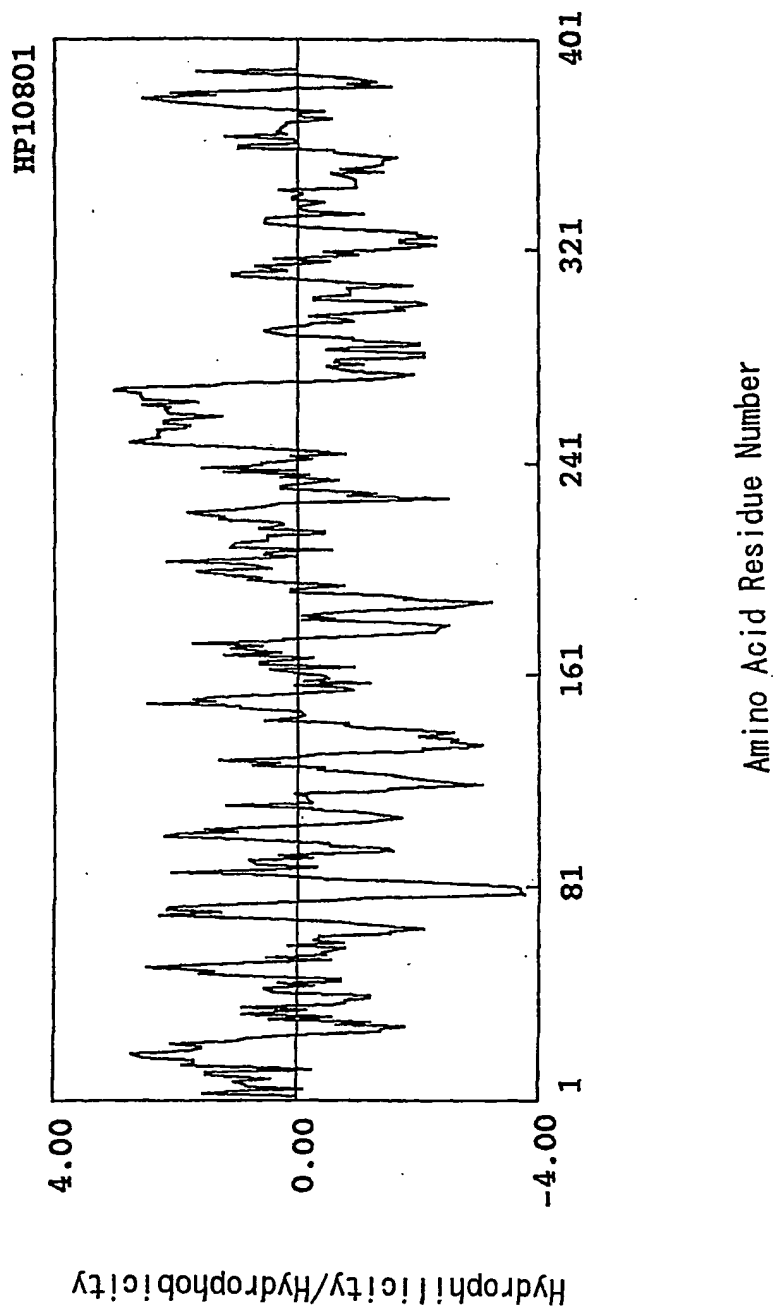
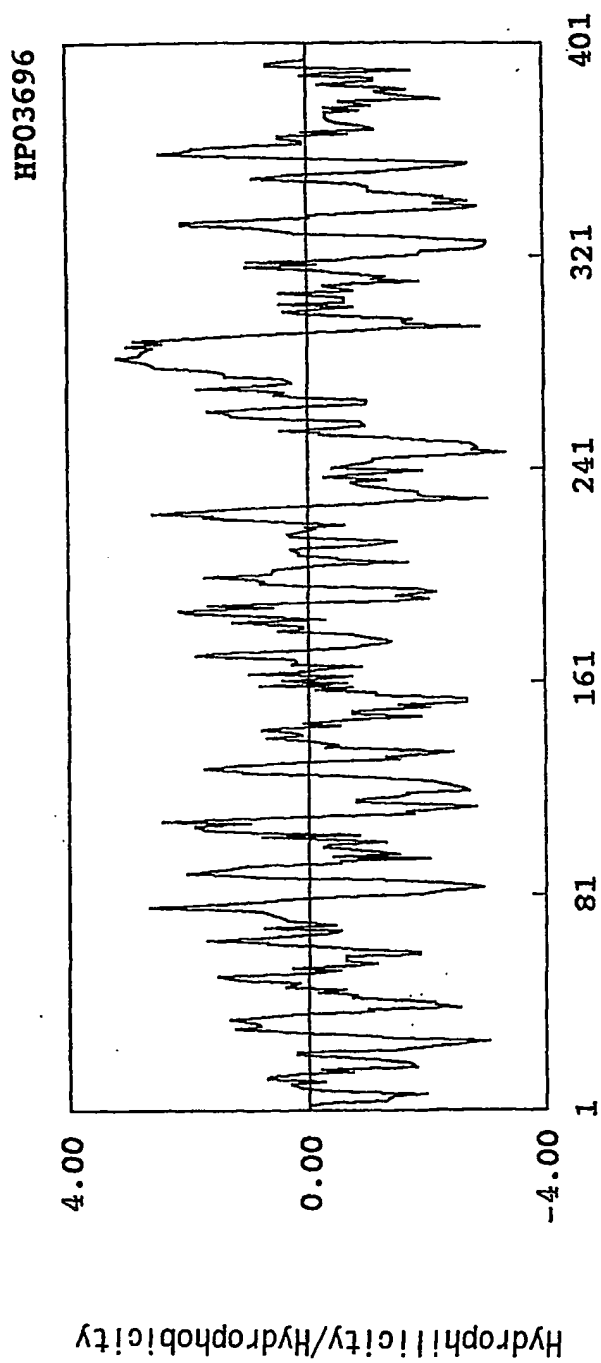


Fig. 40

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Amino Acid Residue Number

Fig. 41

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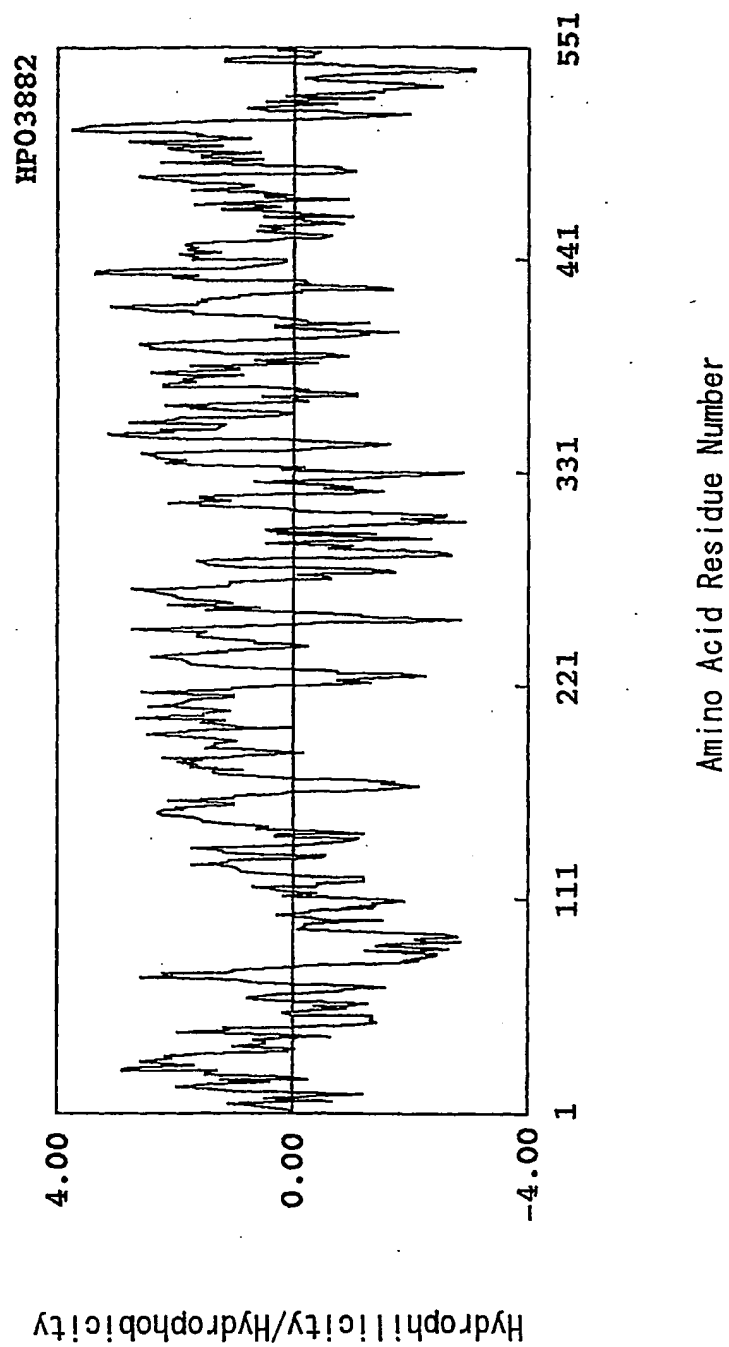


Fig. 42

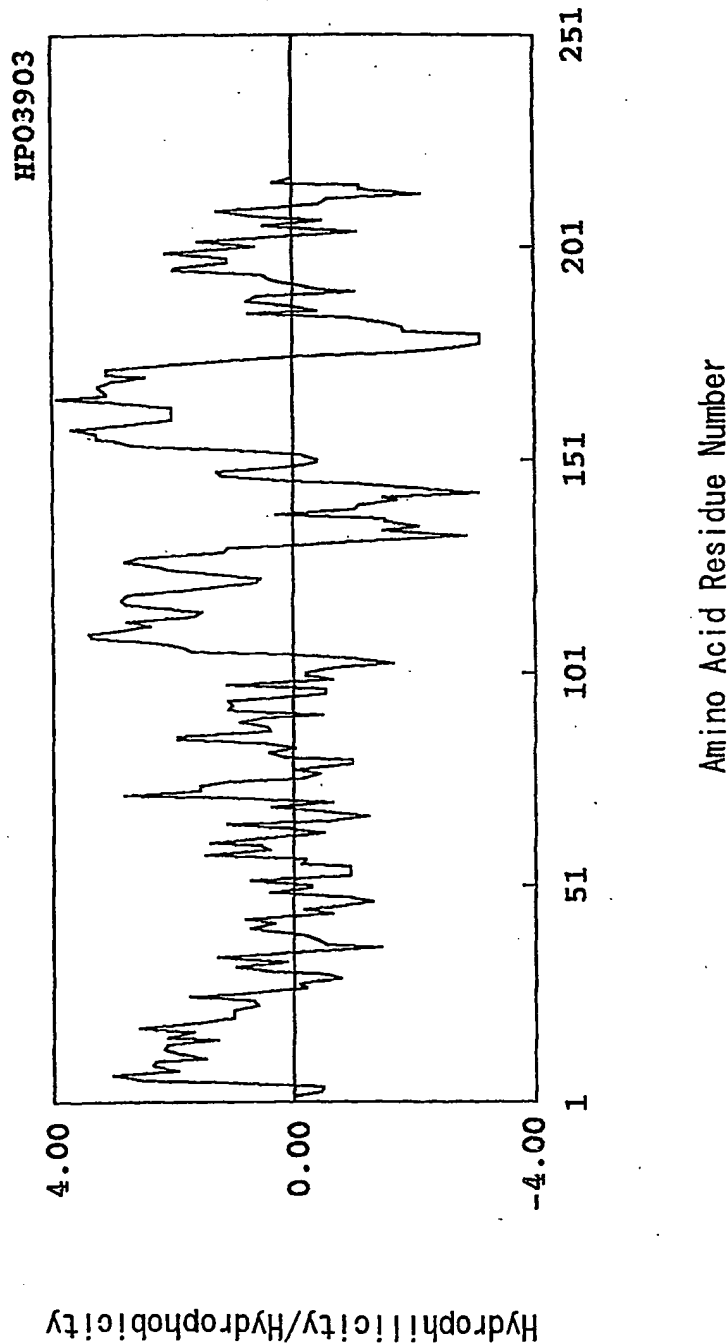


Fig. 43

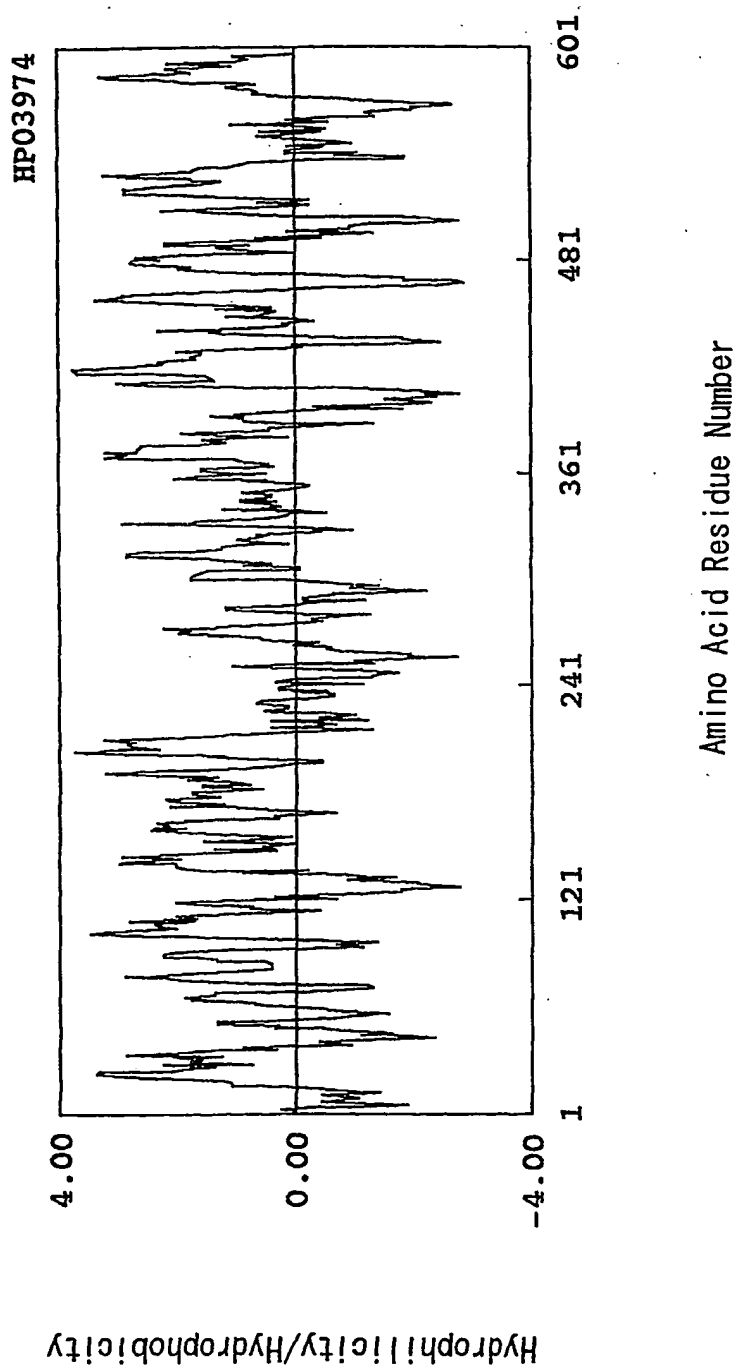


Fig. 44

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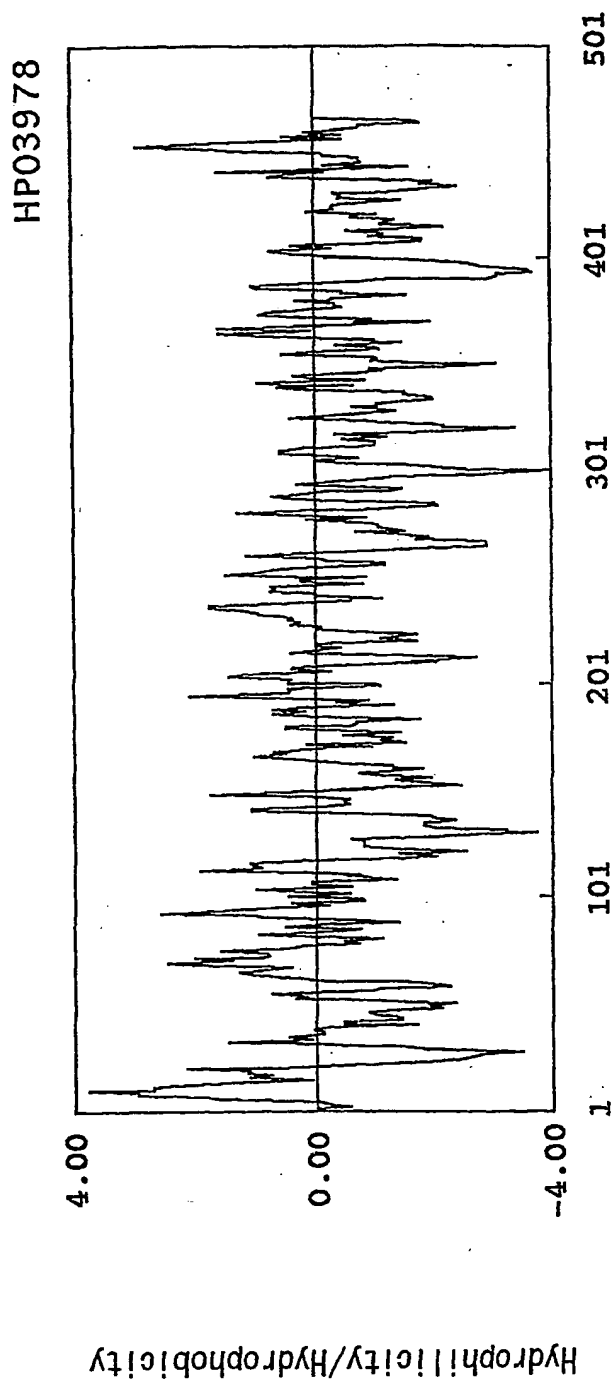
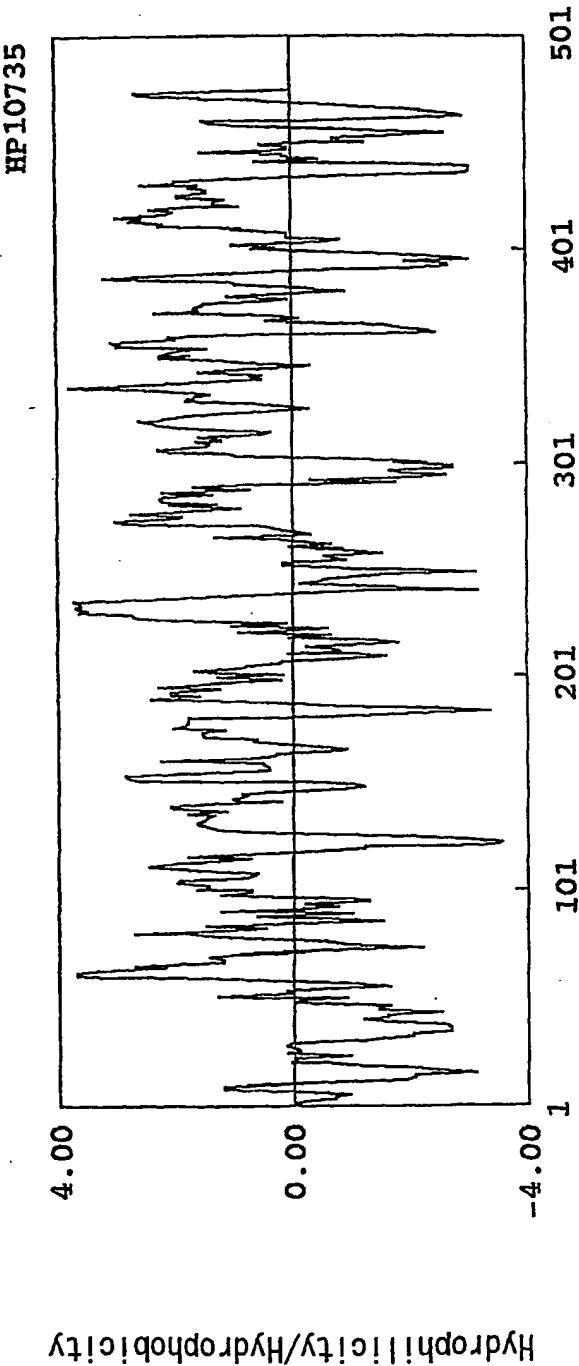


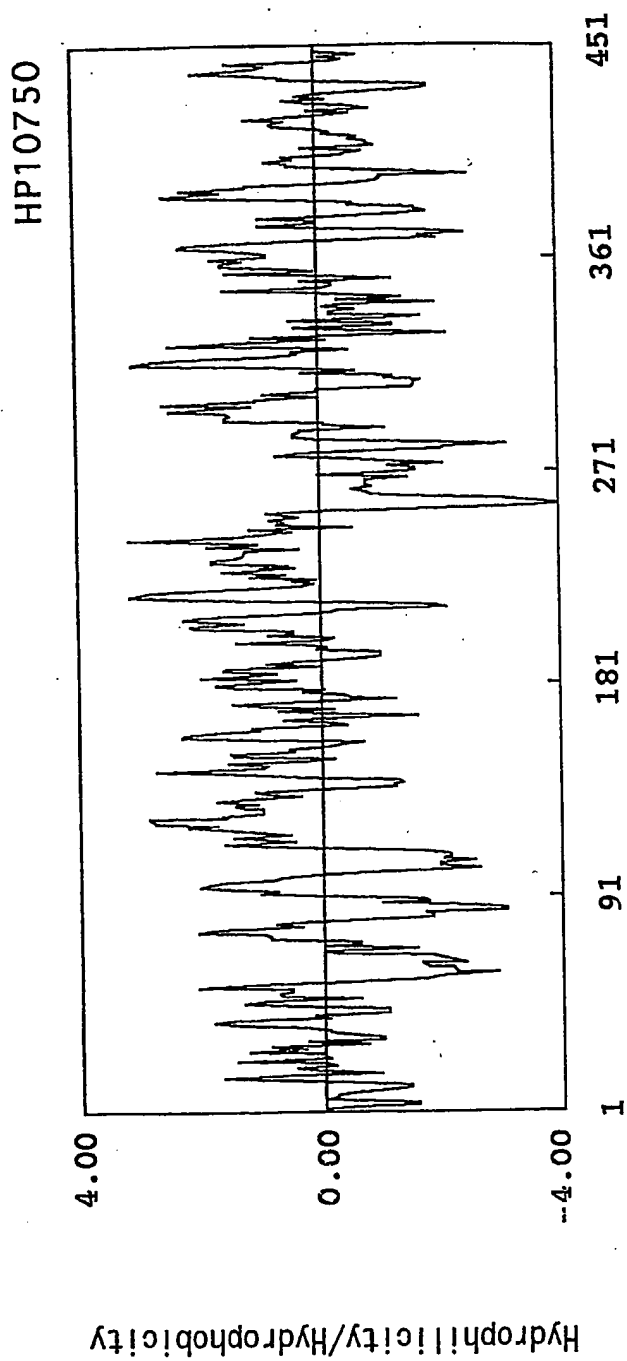
Fig. 45



Amino Acid Residue Number

Fig. 46

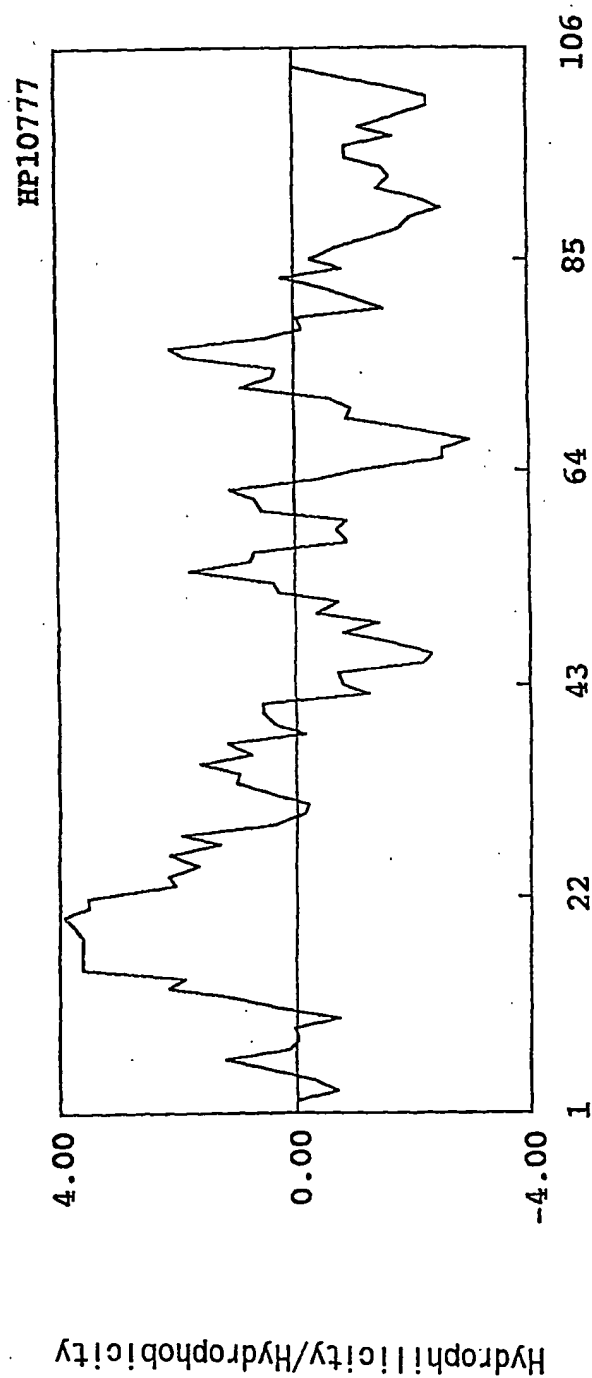
47/50



Amino Acid Residue Number

Fig. 47

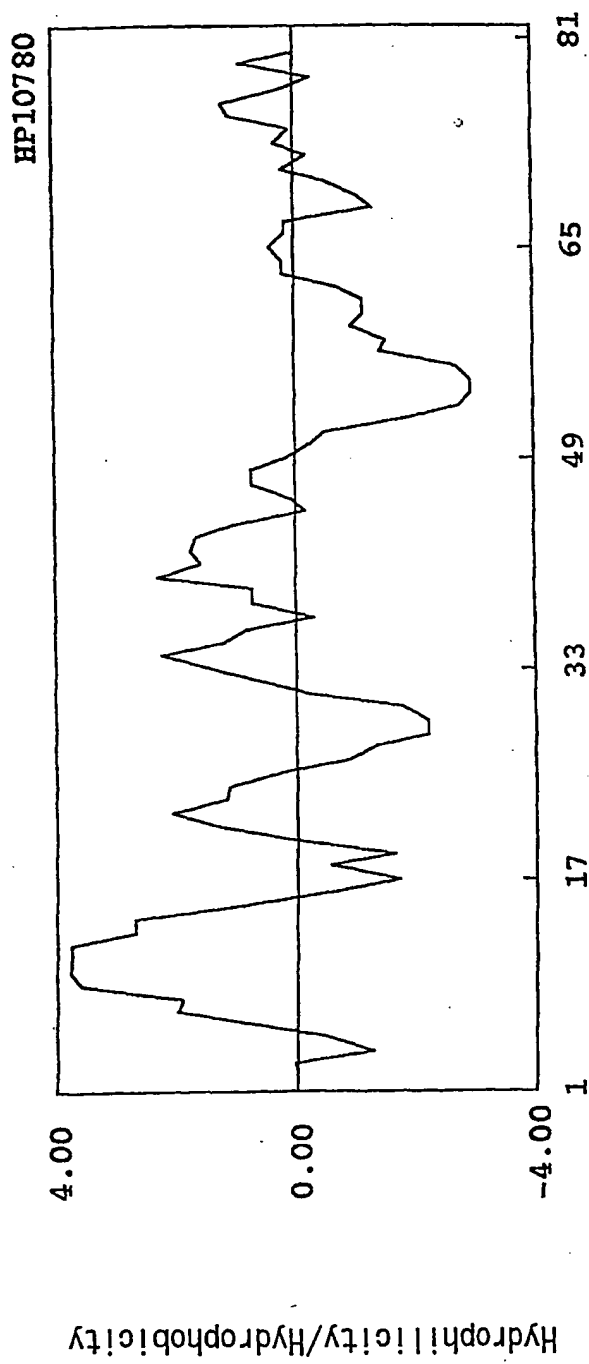
48/50



Amino Acid Residue Number

Fig. 48

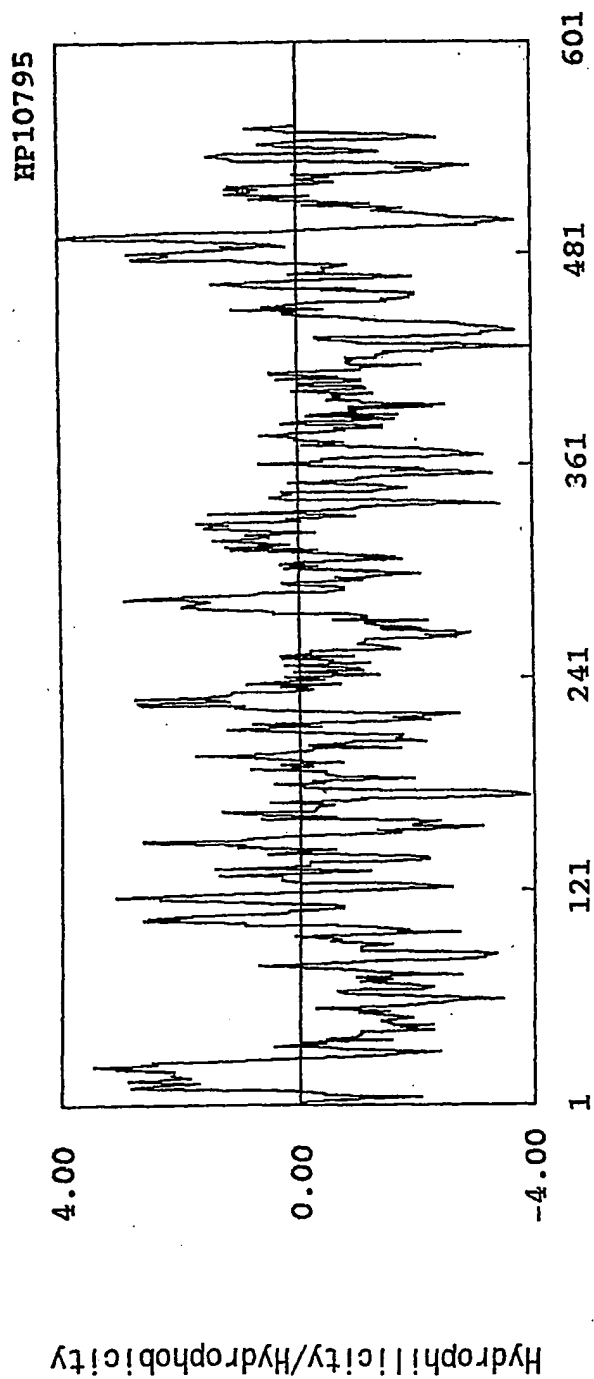
49/50



Amino Acid Residue Number

Fig. 49

50/50



Amino Acid Residue Number

Fig. 50

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SEQUENCE LISTING

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Sagami Chemical Research Center

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Thr Gln Ser Met Leu Glu Asn Phe Ser Ala Ala Val Pro Ser His Arg
35 40 45
Cys Trp Ala Pro Leu Leu Asp Asn Ser Thr Ala Gln Ala Ser Ile Leu
15 50 55 60
Gly Ser Leu Ser Pro Glu Ala Leu Leu Ala Ile Ser Ile Pro Pro Gly
65 70 75 80
Pro Asn Gln Arg Pro His Gln Cys Arg Arg Phe Arg Gln Pro Gln Trp
85 90 95
20 Gln Leu Leu Asp Pro Asn Ala Thr Ala Thr Ser Trp Ser Glu Ala Asp
100 105 110
Thr Glu Pro Cys Val Asp Gly Trp Val Tyr Asp Arg Ser Ile Phe Thr
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Ser Thr Ile Val Ala Lys Trp Asn Leu Val Cys Asp Ser His Ala Leu
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•

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Lys Pro Met Ala Gln Ser Ile Tyr Leu Ala Gly Ile Leu Val Gly Ala
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 Ala Ala Cys Gly Pro Ala Ser Asp Arg Phe Gly Arg Arg Leu Val Leu
 165 170 175
 5 Thr Trp Ser Tyr Leu Gln Met Ala Val Met Gly Thr Ala Ala Ala Phe
 180 185 190
 Ala Pro Ala Phe Pro Val Tyr Cys Leu Phe Arg Phe Leu Leu Ala Phe
 195 200 205
 Ala Val Ala Gly Val Met Met Asn Thr Gly Thr Leu Arg Arg Ser Leu
 10 210 215 220
 Thr Trp Arg His Ala Gly Gly Leu His Ala Gly Ser Arg Ala Glu Pro
 225 230 235 240
 Leu Gly Leu Leu Ala Val Met Glu Trp Thr Ala Ala Arg Ala Arg Pro
 245 250 255
 15 Leu Val Met Thr Leu Asn Ser Leu Gly Phe Ser Phe Gly His Gly Leu
 260 265 270
 Thr Ala Ala Val Ala Tyr Gly Val Arg Asp Trp Thr Leu Leu Gln Leu
 275 280 285
 Val Val Ser Val Pro Phe Phe Leu Cys Phe Leu Tyr Ser Trp Trp Leu
 20 290 295 300
 Ala Glu Ser Ala Arg Trp Leu Leu Thr Thr Gly Arg Leu Asp Trp Gly
 305 310 315 320
 Leu Gln Glu Leu Trp Arg Val Ala Ala Ile Asn Gly Lys Gly Ala Val
 325 330 335
 25 Gln Asp Thr Leu Thr Pro Glu Val Leu Leu Ser Ala Met Arg Glu Glu

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	Pro Gly Leu Arg Phe Arg Thr Cys Ile Ser Thr Leu Cys Trp Phe Ala				
5	370		375		380
	Phe Gly Phe Thr Phe Phe Gly Leu Ala Leu Asp Leu Gln Ala Leu Gly				
	385		390		395
	Ser Asn Ile Phe Leu Leu Gln Met Phe Ile Gly Val Val Asp Ile Pro				
	405		410		415
10	Ala Lys Met Gly Ala Leu Leu Leu Leu Ser His Leu Gly Arg Arg Pro				
	420		425		430
	Thr Leu Ala Ala Ser Leu Leu Leu Ala Gly Leu Cys Ile Leu Ala Asn				
	435		440		445
	Thr Leu Val Pro His Glu Met Gly Ala Leu Arg Ser Ala Leu Ala Val				
15	450		455		460
	Leu Gly Leu Gly Gly Val Gly Ala Ala Phe Thr Cys Ile Thr Ile Tyr				
	465		470		475
	Ser Ser Glu Leu Phe Pro Thr Val Leu Arg Met Thr Ala Val Gly Leu				
	485		490		495
20	Gly Gln Met Ala Ala Arg Gly Gly Ala Ile Leu Gly Pro Leu Val Arg				
	500		505		510
	Leu Leu Gly Val His Gly Pro Trp Leu Pro Leu Leu Val Tyr Gly Thr				
	515		520		525
	Val Pro Val Leu Ser Gly Leu Ala Ala Leu Leu Leu Pro Glu Thr Gln				
25	530		535		540

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Lys Lys Ala Thr His Gly Thr Leu Gly Asn Ser Val Leu Lys Ser Thr
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5 Gln Phe
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Thr His Ser Trp Asp Pro Leu Cys Gly Ser Leu Pro Trp Gly Leu Ser
35 40 45
Cys Leu Leu Ala Leu Gln His Val Leu Val Met Ala Ser Leu Leu Cys
50 55 60
20 Val Ser His Leu Leu Leu Leu Cys Ser Leu Ser Pro Gly Gly Leu Ser
65 70 75 80
Tyr Ser Pro Ser Gln Leu Leu Ala Ser Ser Phe Phe Ser Cys Gly Met
85 90 95
Ser Thr Ile Leu Gln Thr Trp Met Gly Ser Arg Leu Pro Leu Val Gln
25 100 105 110

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Ala Pro Ser Leu Glu Phe Leu Ile Pro Ala Leu Val Leu Thr Ser Gln
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Lys Leu Pro Arg Ala Ile Gln Thr Pro Gly Asn Ser Ser Leu Met Leu
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5 His Leu Cys Arg Gly Pro Ser Cys His Gly Leu Gly His Trp Asn Thr
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Ser Leu Gln Glu Val Ser Gly Ala Val Val Val Ser Gly Leu Leu Gln
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Gly Met Met Gly Leu Leu Gly Ser Pro Gly His Val Phe Pro His Cys
 10 180 185 190

Gly Pro Leu Val Leu Ala Pro Ser Leu Val Val Ala Gly Leu Ser Ala
 195 200 205

His Arg Glu Val Ala Gln Phe Cys Phe Thr His Trp Gly Leu Ala Leu
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Trp Gly Asp

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<212> PRT

<213> Homo sapiens

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 5 Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp Ala
 50 55 60
 Glu Val Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln
 65 70 75 80
 Pro Gly Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln
 10 85 90 95
 Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn
 100 105 110
 Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser
 115 120 125
 15 Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met
 130 135 140
 Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg Leu
 145 150 155 160
 Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn Val
 20 165 170 175
 Val Ile Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys Phe
 180 185 190
 Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe Asp
 195 200 205
 25 Leu Glu Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu Ser

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	Phe Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu Pro			
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	Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser Ser			
5	245	250	255	
	Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu Gln Lys			
	260	265	270	
	Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala Lys Lys Lys			
	275	280	285	
10	Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe Pro Tyr Ala Gln			
	290	295	300	
	Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val Leu Arg Thr Leu Val			
	305	310	315	320
	Gln Glu Lys Gly Thr Glu Val Leu Ala Val Arg Val Val Thr Leu Leu			
15	325	330	335	
	Tyr Asp Leu Val Thr Glu Lys Met Phe Ala Glu Glu Glu Ala Glu Leu			
	340	345	350	
	Thr Gln Glu Met Ser Pro Glu Lys Leu Gln Gln Tyr Arg Gln Val His			
	355	360	365	
20	Leu Leu Pro Gly Leu Trp Glu Gln Gly Trp Cys Glu Ile Thr Ala His			
	370	375	380	
	Leu Leu Ala Leu Pro Glu His Asp Ala Arg Glu Lys Val Leu Gln Thr			
	385	390	395	400
	Leu Gly Val Leu Leu Thr Thr Cys Arg Asp Arg Tyr Arg Gln Asp Pro			
25	405	410	415	

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Gln Leu Gly Arg Thr Leu Ala Ser Leu Gln Ala Glu Tyr Gln Val Leu
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Ala Ser Leu Glu Leu Gln Asp Gly Glu Asp Glu Gly Tyr Phe Gln Glu
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5 Leu Leu Gly Ser Val Asn Ser Leu Leu Lys Glu Leu Arg
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35 40 45
Asn Thr Leu Ala Asp Arg Val His Cys Thr Asn Gly Pro Cys Gly Lys
20 50 55 60
Cys Leu Ser Val Glu Asp Ala Leu Gly Leu Gly Glu Pro Glu Gly Ser
65 70 75 80
Gly Leu Pro Pro Gly Pro Val Leu Glu Ala Arg Tyr Val Ala Arg Leu
85 90 95
25 Ser Ala Ala Ala Val Leu Tyr Leu Ser Asn Pro Glu Gly Thr Cys Glu

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	100	105	110
	Asp Thr Arg Ala Gly Leu Trp Ala Ser His Ala Asp His Leu Leu Ala		
	115	120	125
	Leu Leu Glu Ser Pro Lys Ala Leu Thr Pro Gly Leu Ser Trp Leu Leu		
5	130	135	140
	Gln Arg Met Gln Ala Arg Ala Ala Gly Gln Thr Pro Lys Thr Ala Cys		
	145	150	155
	Val Asp Ile Pro Gln Leu Leu Glu Glu Ala Val Gly Ala Gly Ala Pro		
	165	170	175
10	Gly Ser Ala Gly Gly Val Leu Ala Ala Leu Leu Asp His Val Arg Ser		
	180	185	190
	Gly Ser Cys Phe His Ala Leu Pro Ser Pro Gln Tyr Phe Val Asp Phe		
	195	200	205
	Val Phe Gln Gln His Ser Ser Glu Val Pro Met Thr Leu Ala Glu Leu		
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	Ser Ala Leu Met Gln Arg Leu Gly Val Gly Arg Glu Ala His Ser Asp		
	225	230	235
	His Ser His Arg His Arg Gly Ala Ser Ser Arg Asp Pro Val Pro Leu		
	245	250	255
20	Ile Ser Ser Ser Asn Ser Ser Ser Val Trp Asp Thr Val Cys Leu Ser		
	260	265	270
	Ala Arg Asp Val Met Ala Ala Tyr Gly Leu Ser Glu Gln Ala Gly Val		
	275	280	285
	Thr Pro Glu Ala Trp Ala Gln Leu Ser Pro Ala Leu Leu Gln Gln Gln		
25	290	295	300

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 Leu Ser Gln Ser Glu Arg Tyr Leu Tyr Gly Ser Leu Ala Thr Leu Leu
 325 330 335
 5 Ile Cys Leu Cys Ala Val Phe Gly Leu Leu Leu Leu Thr Cys Thr Gly
 340 345 350
 Cys Arg Gly Val Ala His Tyr Ile Leu Gln Thr Phe Leu Ser Leu Ala
 355 360 365
 Val Gly Ala Leu Thr Gly Asp Ala Val Leu His Leu Thr Pro Lys Val
 10 370 375 380
 Leu Gly Leu His Thr His Ser Glu Glu Gly Leu Ser Pro Gln Pro Thr
 385 390 395 400
 Trp Arg Leu Leu Ala Met Leu Ala Gly Leu Tyr Ala Phe Phe Leu Phe
 405 410 415
 15 Glu Asn Leu Phe Asn Leu Leu Leu Pro Arg Asp Pro Glu Asp Leu Glu
 420 425 430
 Asp Gly Pro Cys Gly His Ser Ser His Ser His Gly Gly His Ser His
 435 440 445
 Gly Val Ser Leu Gln Leu Ala Pro Ser Glu Leu Arg Gln Pro Lys Pro
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 Pro His Glu Gly Ser Arg Ala Asp Leu Val Ala Glu Glu Ser Pro Glu
 465 470 475 480
 Leu Leu Asn Pro Glu Pro Arg Arg Leu Ser Pro Glu Leu Arg Leu Leu
 485 490 495
 25 Pro Tyr Met Ile Thr Leu Gly Asp Ala Val His Asn Phe Ala Asp Gly

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Leu Ala Val Gly Ala Ala Phe Ala Ser Ser Trp Lys Thr Gly Leu Ala
515 520 525
Thr Ser Leu Ala Val Phe Cys His Glu Leu Pro His Glu Leu Gly Asp
5 530 535 540
Phe Ala Ala Leu Leu His Ala Gly Leu Ser Val Arg Gln Ala Leu Leu
545 550 555 560
Leu Asn Leu Ala Ser Ala Leu Thr Ala Phe Ala Gly Leu Tyr Val Ala
565 570 575
10 Leu Ala Val Gly Val Ser Glu Glu Ser Glu Ala Trp Ile Leu Ala Val
580 585 590
Ala Thr Gly Leu Phe Leu Tyr Val Ala Leu Cys Asp Met Leu Pro Ala
595 600 605
Met Leu Lys Val Arg Asp Pro Arg Pro Trp Leu Leu Phe Leu Leu His
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Tyr Glu Asp Asp Ile Thr Phe
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 5 Leu Gln Glu Gln Ala Pro Met Ala Gly Ala Leu Asn Arg Lys Glu Ser
 35 40 45
 Phe Leu Leu Leu Ser Leu His Asn Arg Leu Arg Ser Trp Val Gln Pro
 50 55 60
 Pro Ala Ala Asp Met Arg Arg Leu Asp Trp Ser Asp Ser Leu Ala Gln
 10 65 70 75 80
 Leu Ala Gln Ala Arg Ala Ala Leu Cys Gly Ile Pro Thr Pro Ser Leu
 85 90 95
 Ala Ser Gly Leu Trp Arg Thr Leu Gln Val Gly Trp Asn Met Gln Leu
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 15 Leu Pro Ala Gly Leu Ala Ser Phe Val Glu Val Val Ser Leu Trp Phe
 115 120 125
 Ala Glu Gly Gln Arg Tyr Ser His Ala Ala Gly Glu Cys Ala Arg Asn
 130 135 140
 Ala Thr Cys Thr His Tyr Thr Gln Leu Val Trp Ala Thr Ser Ser Gln
 20 145 150 155 160
 Leu Gly Cys Gly Arg His Leu Cys Ser Ala Gly Gln Ala Ala Ile Glu
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 Ala Phe Val Cys Ala Tyr Ser Pro Gly Gly Asn Trp Glu Val Asn Gly
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 25 Lys Thr Ile Ile Pro Tyr Lys Lys Gly Ala Trp Cys Ser Leu Cys Thr

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	Cys Glu Val Pro Arg Asn Pro Cys Arg Met Ser Cys Gln Asn His Gly		
5	225	230	235
	Arg Leu Asn Ile Ser Thr Cys His Cys His Cys Pro Pro Gly Tyr Thr		
	245	250	255
	Gly Arg Tyr Cys Gln Val Arg Cys Ser Leu Gln Cys Val His Gly Arg		
	260	265	270
10	Phe Arg Glu Glu Glu Cys Ser Cys Val Cys Asp Ile Gly Tyr Gly Gly		
	275	280	285
	Ala Gln Cys Ala Thr Lys Val His Phe Pro Phe His Thr Cys Asp Leu		
	290	295	300
	Arg Ile Asp Gly Asp Cys Phe Met Val Ser Ser Glu Ala Asp Thr Tyr		
15	305	310	315
	Tyr Arg Ala Arg Met Lys Cys Gln Arg Lys Gly Gly Val Leu Ala Gln		
	325	330	335
	Ile Lys Ser Gln Lys Val Gln Asp Ile Leu Ala Phe Tyr Leu Gly Arg		
	340	345	350
20	Leu Glu Thr Thr Asn Glu Val Ile Asp Ser Asp Phe Glu Thr Arg Asn		
	355	360	365
	Phe Trp Ile Gly Leu Thr Tyr Lys Thr Ala Lys Asp Ser Phe Arg Trp		
	370	375	380
	Ala Thr Gly Glu His Gln Ala Phe Thr Ser Phe Ala Phe Gly Gln Pro		
25	385	390	395
			400

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Asp Asn His Gly Phe Gly Asn Cys Val Glu Leu Gln Ala Ser Ala Ala
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 Phe Asn Trp Asn Asn Gln Arg Cys Lys Thr Arg Asn Arg Tyr Ile Cys
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 5 Gln Phe Ala Gln Glu His Ile Ser Arg Trp Gly Pro Gly Ser
 435 440 445

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 35 40 45
 Phe Phe Thr Phe Cys Cys Gly Thr Cys Tyr His Arg Tyr Cys Cys Arg
 20 50 55 60
 Asp Leu Thr Leu Leu Ile Thr Glu Arg Gln Gln Lys His Cys Leu Ala
 65 70 75 80
 Phe Ser Pro Lys Thr Ile Ala Gly Ile Ala Ser Ala Val Ile Leu Phe
 85 90 95
 25 Val Ala Val Val Ala Thr Thr Ile Cys Cys Phe Leu Cys Ser Cys Cys

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 Glu Ile Pro Met Thr Gly Ile Pro Val Gln Pro Val Tyr Pro Tyr Pro
 5 130 135 140
 Gln Asp Pro Lys Ala Gly Pro Ala Pro Pro Gln Pro Gly Phe Ile Tyr
 145 150 155 160
 Pro Pro Ser Gly Pro Ala Pro Gln Tyr Pro Leu Tyr Pro Ala Gly Pro
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 10 Pro Val Tyr Asn Pro Ala Ala Pro Pro Pro Tyr Met Pro Pro Gln Pro
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 Ser Tyr Pro Gly Ala
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 Val Arg Lys Tyr Gln Ser Arg Arg Glu Ser Glu Val Val Ser Thr Ile
 25 35 40 45

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Thr Ala Ile Phe Ser Leu Ala Ile Ala Leu Ile Thr Ser Ala Leu Leu
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 Pro Val Asp Ile Phe Leu Val Ser Tyr Met Lys Asn Gln Asn Gly Thr
 65 70 75 80
 5 Phe Lys Asp Trp Ala Asn Ala Asn Val Ser Arg Gln Ile Glu Asp Thr
 85 90 95
 Val Leu Tyr Gly Tyr Tyr Thr Leu Tyr Ser Val Ile Leu Phe Cys Val
 100 105 110
 Phe Phe Trp Ile Pro Phe Val Tyr Phe Tyr Tyr Glu Glu Lys Asp Asp
 10 115 120 125
 Asp Asp Thr Ser Lys Cys Thr Gln Ile Lys Thr Ala Leu Lys Tyr Thr
 130 135 140
 Leu Gly Phe Val Val Ile Cys Ala Leu Leu Leu Leu Val Gly Ala Phe
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 15 Val Pro Leu Asn Val Pro Asn Asn Lys Asn Ser Thr Glu Trp Glu Lys
 165 170 175
 Val Lys Ser Leu Phe Glu Glu Leu Gly Ser Ser His Gly Leu Ala Ala
 180 185 190
 Leu Ser Phe Ser Ile Ser Ser Leu Thr Leu Ile Gly Met Leu Ala Ala
 20 195 200 205
 Ile Thr Tyr Thr Ala Tyr Gly Met Ser Ala Leu Pro Leu Asn Leu Ile
 210 215 220
 Lys Gly Thr Arg Ser Ala Ala Tyr Glu Arg Leu Glu Asn Thr Glu Asp
 225 230 235 240
 25 Ile Glu Glu Val Glu Gln His Ile Gln Thr Ile Lys Ser Lys Ser Lys

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	245	250	255
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	Glu Glu Arg Leu Arg Thr Leu Lys Lys Arg Glu Arg His Leu Glu Phe		
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	Ile Glu Asn Ser Trp Trp Thr Lys Phe Cys Gly Ala Leu Arg Pro Leu		
	290	295	300
	Lys Ile Val Trp Gly Ile Phe Phe Ile Leu Val Ala Leu Leu Phe Val		
	305	310	315
10	Ile Ser Leu Phe Leu Ser Asn Leu Asp Lys Ala Leu His Ser Ala Gly		
	325	330	335
	Ile Asp Ser Gly Phe Ile Ile Phe Gly Ala Asn Leu Ser Asn Pro Leu		
	340	345	350
	Asn Met Leu Leu Pro Leu Leu Gln Thr Val Phe Pro Leu Asp Tyr Ile		
15	355	360	365
	Leu Ile Thr Ile Ile Ile Met Tyr Phe Ile Phe Thr Ser Met Ala Gly		
	370	375	380
	Ile Arg Asn Ile Gly Ile Trp Phe Phe Trp Ile Arg Leu Tyr Lys Ile		
	385	390	395
20	Arg Arg Gly Arg Thr Arg Pro Gln Ala Leu Leu Phe Leu Cys Met Ile		
	405	410	415
	Leu Leu Leu Ile Val Leu His Thr Ser Tyr Met Ile Tyr Ser Leu Ala		
	420	425	430
	Pro Gln Tyr Val Met Tyr Gly Ser Gln Asn Tyr Leu Ile Glu Thr Asn		
25	435	440	445

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Ile Thr Ser Asp Asn His Lys Gly Asn Ser Thr Leu Ser Val Pro Lys
 450 455 460
 Arg Cys Asp Ala Asp Ala Pro Glu Asp Gln Cys Thr Val Thr Arg Thr
 465 470 475 480
 5 Tyr Leu Phe Leu His Lys Phe Trp Phe Phe Ser Ala Ala Tyr Tyr Phe
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 Gly Asn Trp Ala Phe Leu Gly Val Phe Leu Ile Gly Leu Ile Val Ser
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 35 40 45
 25 Arg Ala Val Leu Arg Cys Gln Ser Pro Arg Met Val Trp Thr Gln Asp

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50 55 60
Arg Leu His Asp Arg Gln Arg Val Leu His Trp Asp Leu Arg Gly Pro
65 70 75 80
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5 85 90 95
Gln Arg Val Tyr Glu Ala Arg Asp Arg Gly Arg Leu Glu Leu Ser Ala
100 105 110
Ser Ala Phe Asp Asp Gly Asn Phe Ser Leu Leu Ile Arg Ala Val Glu
115 120 125
10 Glu Thr Asp Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys
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His Leu Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro
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Pro Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
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Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His Val
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Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His Trp Asp
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20 Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg Leu Leu Asp
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225 230 235 240
Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu Arg Gly Asp Phe Ser
25 245 250 255

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 His Leu His His His Tyr Cys Gly Leu His Glu Arg Arg Val Phe His
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 Gly Asn Gly Ser Ser His Ser Gly Ala Pro Gly Pro Asp Pro Thr Leu
 305 310 315 320
 Ala Arg Gly His Asn Val Ile Asn Val Ile Val Pro Glu Ser Arg Ala
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 355 360 365
 15 Gly Tyr Glu Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp
 370 375 380
 Val Asn Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr
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 Arg Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu
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25

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<210> 9

<211> 262

<212> PRT

<213> Homo sapiens

5 <400> 9

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10 Ala Ala Leu Gly Pro Leu Ser Phe Gly Phe Ala Leu Gly Tyr Ser Ser

35 40 45

Pro Ala Ile Pro Ser Leu Gln Arg Ala Ala Pro Pro Ala Pro Arg Leu

50 55 60

Asp Asp Ala Ala Ala Ser Trp Phe Gly Ala Val Val Thr Leu Gly Ala

15 65 70 75 80

Ala Ala Gly Gly Val Leu Gly Gly Trp Leu Val Asp Arg Ala Gly Arg

85 90 95

Lys Leu Ser Leu Leu Leu Cys Ser Val Pro Phe Val Ala Gly Phe Ala

100 105 110

20 Val Ile Thr Ala Ala Gln Asp Val Trp Met Leu Leu Gly Gly Arg Leu

115 120 125

Leu Thr Gly Leu Ala Cys Gly Val Ala Ser Leu Val Ala Pro Val Tyr

130 135 140

Ile Ser Glu Ile Ala Tyr Pro Ala Val Arg Gly Leu Leu Gly Ser Cys

25 145 150 155 160

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Val Gln Leu Met Val Val Val Gly Ile Leu Leu Ala Tyr Leu Ala Gly
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 180 185 190
 5 Ser Leu Met Leu Leu Leu Met Cys Phe Met Pro Glu Thr Pro Arg Phe
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 Leu Leu Thr Gln His Arg Arg Gln Glu Ala Ala Pro Gly Leu Val Arg
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 Cys Gly His Gly Val Gln His Glu Cys Leu Arg Arg Leu Leu Gln Ala
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 85 90 95
 Phe Leu Lys His Leu Thr Gly Pro Leu Tyr Phe Ser Pro Lys Cys Ser
 100 105 110
 10 Lys His Phe His Arg Leu Tyr His Asn Thr Arg Asp Cys Thr Ile Pro
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<212> DNA

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<211> 732

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5 <213> Homo sapiens

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25 <400> 13

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<211> 1944

<212> DNA

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20 <211> 594

<212> DNA

<213> Homo sapiens

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34 / 346

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Met Ala Phe Ser Glu Leu

1

5

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Leu Asp Leu Val Gly Gly Leu Gly Arg Phe Gln Val Leu Gln Thr Met

25

10

15

20

36 /346

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	Asp Asn Ser Thr Ala Gln Ala Ser Ile Leu Gly Ser Leu Ser Pro Glu	
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	Trp Asn Leu Val Cys Asp Ser His Ala Leu Lys Pro Met Ala Gln Ser	
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	Leu Leu Thr Thr Gly Arg Leu Asp Trp Gly Leu Gln Glu Leu Trp Arg			
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	gtg gct gcc atc aac gga aag ggg gca gtg cag gac acc ctg acc cct	1363		
	Val Ala Ala Ile Asn Gly Lys Gly Ala Val Gln Asp Thr Leu Thr Pro			
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	Glu Val Leu Leu Ser Ala Met Arg Glu Glu Leu Ser Met Gly Gln Pro			
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	cct gcc agc ctg ggc acc ctg ctc cgc atg ccc gga ctg cgc ttc cgg	1459		
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	acc tgt atc tcc acg ttg tgc tgg ttc gcc ttt ggc ttc acc ttc ttc	1507		
	Thr Cys Ile Ser Thr Leu Cys Trp Phe Ala Phe Gly Phe Thr Phe Phe			
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	Thr Val Leu Arg Met Thr Ala Val Gly Leu Gly Gln Met Ala Ala Arg	
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	Gly Gly Ala Ile Leu Gly Pro Leu Val Arg Leu Leu Gly Val His Gly	
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555

560

565

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Thr Leu Gly Asn Ser Val Leu Lys Ser Thr Gln Phe

5

570

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41 / 346

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20

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Ala Pro Leu Pro Pro Pro Ala Pro Gln Asn Pro Ser Thr His Ser Trp

25

30

35

gac cct ttg tgt gga tct ctg cct tgg ggc ctc agc tgt ctt ctg gct 201

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ctg cag cat gtc ttg gtc atg gct tct ctg ctc tgt gtc tcc cac ctg 249

Leu Gln His Val Leu Val Met Ala Ser Leu Leu Cys Val Ser His Leu

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20 Leu Leu Leu Cys Ser Leu Ser Pro Gly Gly Leu Ser Tyr Ser Pro Ser

70

75

80

cag ctc ctg gcc tcc agc ttc ttt tca tgt ggt atg tct acc atc ctg 345

Gln Leu Leu Ala Ser Ser Phe Phe Ser Cys Gly Met Ser Thr Ile Leu

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90

95

100

25 caa act tgg atg ggc agc agg ctg cct ctt gtc cag gct cca tcc tta 393

42 / 346

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Leu Gly Met Leu Leu Gly Leu Leu Met Ala Ala Cys Phe Thr Phe Cys
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Leu Ser His Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys
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agc agc acc aaa gaa aca gag aga aaa gaa acc aaa gcc gag gag gag 255
15 Ser Ser Thr Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu
              50              55              60
ctg gat gcc gaa gtc ctg gag gtg ttc cac ccg acg cat gag tgg cag 303
Leu Asp Ala Glu Val Leu Glu Val Phe His Pro Thr His Glu Trp Gln
              65              70              75
gcc ctt cag cca ggg cag gct gtc cct gca gga tcc cac gta cgg ctg 351
20 Ala Leu Gln Pro Gly Gln Ala Val Pro Ala Gly Ser His Val Arg Leu
              80              85              90
aat ctt cag act ggg gaa aga gag gca aaa ctc caa tat gag gac aag 399
Asn Leu Gln Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys
25      95              100              105

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 Phe Arg Asn Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr
 110 115 120 125
 tac aca tct cag gat ctc aag agt gca ctg gca aaa ttc aag gag ggg 495
 5 Tyr Thr Ser Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly
 130 135 140
 gca gag atg gag agt tca aag gaa gac aag gca agg cag gct gag gta 543
 Ala Glu Met Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val
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 10 aag cgg ctc ttc cgc ccc att gag gaa ctg aag aaa gac ttt gat gag 591
 Lys Arg Leu Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu
 160 165 170
 ctg aat gtt gtc att gag act gac atg cag atc atg gta cgg ctg atc 639
 Leu Asn Val Val Ile Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile
 15 175 180 185
 aac aag ttc aat agt tcc agc tcc agt ttg gaa gag aag att gct gcg 687
 Asn Lys Phe Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala
 190 195 200 205
 ctc ttt gat ctt gaa tat tat gtc cat cag atg gac aat gcg cag gac 735
 20 Leu Phe Asp Leu Glu Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp
 210 215 220
 ctg ctt tcc ttt ggt ggt ctt caa gtg gtg atc aat ggg ctg aac agc 783
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 25 aca gag ccc ctc gtg aag gag tat gct gcg ttt gtg ctg ggc gct gcc 831

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	240					245					250							
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	Phe	Ser	Ser	Asn	Pro	Lys	Val	Gln	Val	Glu	Ala	Ile	Glu	Gly	Gly	Ala		
5	255					260					265							
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	Leu	Gln	Lys	Leu	Leu	Val	Ile	Leu	Ala	Thr	Glu	Gln	Pro	Leu	Thr	Ala		
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	Tyr	Ala	Gln	Arg	Gln	Phe	Leu	Lys	Leu	Gly	Gly	Leu	Gln	Val	Leu	Arg		
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	Thr	Leu	Val	Gln	Glu	Lys	Gly	Thr	Glu	Val	Leu	Ala	Val	Arg	Val	Val		
	320					325					330							
	aca	ctg	ctc	tac	gac	ctg	gtc	acg	gag	aag	atg	ttc	gcc	gag	gag	gag	1119	
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20	335					340					345							
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	Ala	Glu	Leu	Thr	Gln	Glu	Met	Ser	Pro	Glu	Lys	Leu	Gln	Gln	Tyr	Arg		
	350					355					360					365		
	cag	gta	cac	ctc	ctg	cca	ggc	ctg	tgg	gaa	cag	ggc	tgg	tgc	gag	atc	1215	
25	Gln	Val	His	Leu	Leu	Pro	Gly	Leu	Trp	Glu	Gln	Gly	Trp	Cys	Glu	Ile		

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	370	375	380	
	acg gcc cac ctc ctg gcg ctg ccc gag cat gat gcc cgt gag aag gtg	1263		
	Thr Ala His Leu Leu Ala Leu Pro Glu His Asp Ala Arg Glu Lys Val			
	385	390	395	
5	ctg cag aca ctg ggc gtc ctc ctg acc acc tgc cgg gac cgc tac cgt	1311		
	Leu Gln Thr Leu Gly Val Leu Leu Thr Thr Cys Arg Asp Arg Tyr Arg			
	400	405	410	
	cag gac ccc cag ctc ggc agg aca ctg gcc agc ctg cag gct gag tac	1359		
	Gln Asp Pro Gln Leu Gly Arg Thr Leu Ala Ser Leu Gln Ala Glu Tyr			
10	415	420	425	
	cag gtg ctg gcc agc ctg gag ctg cag gat ggt gag gac gag ggc tac	1407		
	Gln Val Leu Ala Ser Leu Glu Leu Gln Asp Gly Glu Asp Glu Gly Tyr			
	430	435	440	445
	ttc cag gag ctg ctg ggc tct gtc aac agc ttg ctg aag gag ctg aga	1455		
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	450	455	460	
	tgaggcccca caccaggact ggactgggat gccgctagtg aggctgaggg gtgccagcgt	1515		
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49 / 346

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<400> 24

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Ala Ser Leu Val Ser Leu Glu Leu Gly Leu Leu Leu Ala Val Leu Val

           5               10               15

10  gtg acg gcg acg gcg tcc ccg cct gct ggt ctg ctg agc ctg ctc acc  154
Val Thr Ala Thr Ala Ser Pro Pro Ala Gly Leu Leu Ser Leu Leu Thr

           20               25               30

tct ggc cag ggc gct ctg gat caa gag gct ctg ggc ggc ctg tta aat  202
Ser Gly Gln Gly Ala Leu Asp Gln Glu Ala Leu Gly Gly Leu Leu Asn

15      35               40               45

acg ctg gcg gac cgt gtg cac tgc acc aac ggg ccg tgt gga aag tgc  250
Thr Leu Ala Asp Arg Val His Cys Thr Asn Gly Pro Cys Gly Lys Cys

      50               55               60               65

ctg tct gtg gag gac gcc ctg ggc ctg ggc gag cct gag ggg tca ggg  298
20  Leu Ser Val Glu Asp Ala Leu Gly Leu Gly Glu Pro Glu Gly Ser Gly

           70               75               80

ctg ccc ccg ggc ccg gtc ctg gag gcc agg tac gtc gcc cgc ctc agt  346
Leu Pro Pro Gly Pro Val Leu Glu Ala Arg Tyr Val Ala Arg Leu Ser

           85               90               95

25  gcc gcc gcc gtc ctg tac ctc agc aac ccc gag ggc acc tgt gag gac  394

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Ala Ala Ala Val Leu Tyr Leu Ser Asn Pro Glu Gly Thr Cys Glu Asp
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Thr Arg Ala Gly Leu Trp Ala Ser His Ala Asp His Leu Leu Ala Leu
5 115 120 125
ctc gag agc ccc aag gcc ctg acc ccg ggc ctg agc tgg ctg ctg cag 490
Leu Glu Ser Pro Lys Ala Leu Thr Pro Gly Leu Ser Trp Leu Leu Gln
130 135 140 145
agg atg cag gcc cgg gct gcc ggc cag acc ccc aag acg gcc tgc gta 538
10 Arg Met Gln Ala Arg Ala Ala Gly Gln Thr Pro Lys Thr Ala Cys Val
150 155 160
gat atc cct cag ctg ctg gag gag gcg gtg ggg gcg ggg gct ccg ggc 586
Asp Ile Pro Gln Leu Leu Glu Glu Ala Val Gly Ala Gly Ala Pro Gly
165 170 175
15 agt gct ggc ggc gtc ctg gct gcc ctg ctg gac cat gtc agg agc ggg 634
Ser Ala Gly Gly Val Leu Ala Ala Leu Leu Asp His Val Arg Ser Gly
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tct tgc ttc cac gcc ttg ccg agc cct cag tac ttc gtg gac ttt gtg 682
Ser Cys Phe His Ala Leu Pro Ser Pro Gln Tyr Phe Val Asp Phe Val
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ttc cag cag cac agc agc gag gtc cct atg acg ctg gcc gag ctg tca 730
Phe Gln Gln His Ser Ser Glu Val Pro Met Thr Leu Ala Glu Leu Ser
210 215 220 225
gcc ttg atg cag cgc ctg ggg gtg ggc agg gag gcc cac agt gac cac 778
25 Ala Leu Met Gln Arg Leu Gly Val Gly Arg Glu Ala His Ser Asp His

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	230	235	240	
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	Ser His Arg His Arg Gly Ala Ser Ser Arg Asp Pro Val Pro Leu Ile			
	245	250	255	
5	agc tcc agc aac agc tcc agt gtg tgg gac acg gta tgc ctg agt gcc			874
	Ser Ser Ser Asn Ser Ser Ser Val Trp Asp Thr Val Cys Leu Ser Ala			
	260	265	270	
	agg gac gtg atg gct gca tat gga ctg tcg gaa cag gct ggg gtg acc			922
	Arg Asp Val Met Ala Ala Tyr Gly Leu Ser Glu Gln Ala Gly Val Thr			
10	275	280	285	
	ccg gag gcc tgg gcc caa ctg agc cct gcc ctg ctc caa cag cag ctg			970
	Pro Glu Ala Trp Ala Gln Leu Ser Pro Ala Leu Leu Gln Gln Gln Leu			
	290	295	300	305
	agt gga gcc tgc acc tcc cag tcc agg ccc ccc gtc cag gac cag ctc			1018
15	Ser Gly Ala Cys Thr Ser Gln Ser Arg Pro Pro Val Gln Asp Gln Leu			
	310	315	320	
	agc cag tca gag agg tat ctg tac ggc tcc ctg gcc acg ctg ctc atc			1066
	Ser Gln Ser Glu Arg Tyr Leu Tyr Gly Ser Leu Ala Thr Leu Leu Ile			
	325	330	335	
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	Cys Leu Cys Ala Val Phe Gly Leu Leu Leu Leu Thr Cys Thr Gly Cys			
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	agg ggg gtc gcc cac tac atc ctg cag acc ttc ctg agc ctg gca gtg			1162
	Arg Gly Val Ala His Tyr Ile Leu Gln Thr Phe Leu Ser Leu Ala Val			
25	355	360	365	

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 Gly Ala Leu Thr Gly Asp Ala Val Leu His Leu Thr Pro Lys Val Leu
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 ggg ctg cat aca cac agc gaa gag ggc ctc agc cca cag ccc acc tgg 1258
 5 Gly Leu His Thr His Ser Glu Glu Gly Leu Ser Pro Gln Pro Thr Trp
 390 395 400
 cgc ctc ctg gct atg ctg gcc ggg ctc tac gcc ttc ttc ctg ttt gag 1306
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 405 410 415
 10 aac ctc ttc aat ctc ctg ctg ccc agg gac ccg gag gac ctg gag gac 1354
 Asn Leu Phe Asn Leu Leu Leu Pro Arg Asp Pro Glu Asp Leu Glu Asp
 420 425 430
 ggg ccc tgc ggc cac agc agc cat agc cac ggg ggc cac agc cac ggt 1402
 Gly Pro Cys Gly His Ser Ser His Ser His Gly Gly His Ser His Gly
 15 435 440 445
 gtg tcc ctg cag ctg gca ccc agc gag ctc cgg cag ccc aag ccc ccc 1450
 Val Ser Leu Gln Leu Ala Pro Ser Glu Leu Arg Gln Pro Lys Pro Pro
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 cac gag ggc tcc cgc gca gac ctg gtg gcg gag gag agc ccg gag ctg 1498
 20 His Glu Gly Ser Arg Ala Asp Leu Val Ala Glu Glu Ser Pro Glu Leu
 470 475 480
 ctg aac cct gag ccc agg aga ctg agc cca gag ttg agg cta ctg ccc 1546
 Leu Asn Pro Glu Pro Arg Arg Leu Ser Pro Glu Leu Arg Leu Leu Pro
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 25 tat atg atc act ctg ggc gac gcc gtg cac aac ttc gcc gac ggg ctg 1594

53 /346

	Tyr Met Ile Thr Leu Gly Asp Ala Val His Asn Phe Ala Asp Gly Leu	
	500	505 510
	gcc gtg ggc gcc gcc ttc gcg tcc tcc tgg aag acc ggg ctg gcc acc	1642
	Ala Val Gly Ala Ala Phe Ala Ser Ser Trp Lys Thr Gly Leu Ala Thr	
5	515 520 525	
	tcg ctg gcc gtg ttc tgc cac gag ttg cca cac gag ctg ggg gac ttc	1690
	Ser Leu Ala Val Phe Cys His Glu Leu Pro His Glu Leu Gly Asp Phe	
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	gcc gcc ttg ctg cac gcg ggg ctg tcc gtg cgc caa gca ctg ctg ctg	1738
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	550 555 560	
	aac ctg gcc tcc gcg ctc acg gcc ttc gct ggt ctc tac gtg gca ctc	1786
	Asn Leu Ala Ser Ala Leu Thr Ala Phe Ala Gly Leu Tyr Val Ala Leu	
	565 570 575	
15	gcg gtt gga gtc agc gag gag agc gag gcc tgg atc ctg gca gtg gcc	1834
	Ala Val Gly Val Ser Glu Glu Ser Glu Ala Trp Ile Leu Ala Val Ala	
	580 585 590	
	acc ggc ctg ttc ctc tac gta gca ctc tgc gac atg ctc ccg gcg atg	1882
	Thr Gly Leu Phe Leu Tyr Val Ala Leu Cys Asp Met Leu Pro Ala Met	
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	ttg aaa gta cgg gac ccg cgg ccc tgg ctc ctc ttc ctg ctg cac aac	1930
	Leu Lys Val Arg Asp Pro Arg Pro Trp Leu Leu Phe Leu Leu His Asn	
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	gtg ggc ctg ctg ggc ggc tgg acc gtc ctg ctg ctg ctg tcc ctg tac	1978
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630 635 640

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Glu Asp Asp Ile Thr Phe

645

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Met Leu His Pro Glu Thr Ser Pro Gly Arg Gly His Leu Leu Ala Val

1 5 10 15

20 ctc ctg gcc ctc ctt ggc acc gcc tgg gca gag gtg tgg cca ccc cag 157

Leu Leu Ala Leu Leu Gly Thr Ala Trp Ala Glu Val Trp Pro Pro Gln

20 25 30

ctg cag gag cag gct ccg atg gcc gga gcc ctg aac agg aag gag agt 205

Leu Gln Glu Gln Ala Pro Met Ala Gly Ala Leu Asn Arg Lys Glu Ser

25 35 40 45

55 /346

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	cct gcg gct gac atg cgg agg ctg gac tgg agt gac agc ctg gcc caa	301
5	Pro Ala Ala Asp Met Arg Arg Leu Asp Trp Ser Asp Ser Leu Ala Gln	
	65 70 75 80	
	ctg gct caa gcc agg gca gcc ctc tgt gga atc cca acc ccg agc ctg	349
	Leu Ala Gln Ala Arg Ala Ala Leu Cys Gly Ile Pro Thr Pro Ser Leu	
	85 90 95	
10	gcg tcc ggc ctg tgg cgc acc ctg caa gtg ggc tgg aac atg cag ctg	397
	Ala Ser Gly Leu Trp Arg Thr Leu Gln Val Gly Trp Asn Met Gln Leu	
	100 105 110	
	ctg ccc gcg ggc ttg gcg tcc ttt gtt gaa gtg gtc agc cta tgg ttt	445
	Leu Pro Ala Gly Leu Ala Ser Phe Val Glu Val Val Ser Leu Trp Phe	
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	gca gag ggg cag cgg tac agc cac gcg gca gga gag tgt gct cgc aac	493
	Ala Glu Gly Gln Arg Tyr Ser His Ala Ala Gly Glu Cys Ala Arg Asn	
	130 135 140	
	gcc acc tgc acc cac tac acg cag ctc gtg tgg gcc acc tca agc cag	541
20	Ala Thr Cys Thr His Tyr Thr Gln Leu Val Trp Ala Thr Ser Ser Gln	
	145 150 155 160	
	ctg ggc tgt ggg cgg cac ctg tgc tct gca ggc cag gca gcg ata gaa	589
	Leu Gly Cys Gly Arg His Leu Cys Ser Ala Gly Gln Ala Ala Ile Glu	
	165 170 175	
25	gcc ttt gtc tgt gcc tac tcc ccc gga ggc aac tgg gag gtc aac ggg	637

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5 195 200 205
gcc agt gtc tca ggc tgc ttc aaa gcc tgg gac cat gca ggg ggg ctc 733
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10 Cys Glu Val Pro Arg Asn Pro Cys Arg Met Ser Cys Gln Asn His Gly
225 230 235 240
cgt ctc aac atc agc acc tgc cac tgc cac tgt ccc cct ggc tac acg 829
Arg Leu Asn Ile Ser Thr Cys His Cys His Cys Pro Pro Gly Tyr Thr
245 250 255
15 ggc aga tac tgc caa gtg agg tgc agc ctg cag tgt gtg cac ggc cgg 877
Gly Arg Tyr Cys Gln Val Arg Cys Ser Leu Gln Cys Val His Gly Arg
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ttc cgg gag gag gag tgc tcg tgc gtc tgt gac atc ggc tac ggg gga 925
Phe Arg Glu Glu Glu Cys Ser Cys Val Cys Asp Ile Gly Tyr Gly Gly
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gcc cag tgt gcc acc aag gtg cat ttt ccc ttc cac acc tgt gac ctg 973
Ala Gln Cys Ala Thr Lys Val His Phe Pro Phe His Thr Cys Asp Leu
290 295 300
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25 Arg Ile Asp Gly Asp Cys Phe Met Val Ser Ser Glu Ala Asp Thr Tyr

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	Ile Lys Ser Gln Lys Val Gln Asp Ile Leu Ala Phe Tyr Leu Gly Arg				
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	Leu Glu Thr Thr Asn Glu Val Ile Asp Ser Asp Phe Glu Thr Arg Asn				
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		370	375	380	
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	Phe Asn Trp Asn Asn Gln Arg Cys Lys Thr Arg Asn Arg Tyr Ile Cys				
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	cag ttt gcc cag gag cac atc tcc cgg tgg ggc cca ggg tcc	1399			
	Gln Phe Ala Gln Glu His Ile Ser Arg Trp Gly Pro Gly Ser				
25		435	440	445	

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 5 tcaattagat ggcaaaggag aggacaccgc cagtgttcca aaaaggctgc tctcttcac 1699
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 tcgctggtgg gtggactcct gggcgctgcy cggagccgcy ccggctgggt tagcgcgggc 180
 20 ggggcgctta gtcccacccc cagaggaggc ggaagaggag ccgagcctg gccgcgggct 240
 gggccccgcc gcagctccag ctggccggct tggctctgcy gtcccttctc tgggaggccc 300
 gaccccgccc gcgccagcc ccacc atg cca ccc gcg ggg ctc cgc cgg gcc 353

Met Pro Pro Ala Gly Leu Arg Arg Ala

1

5

25 gcg ccg ctc acc gca atc gct ctg ttg gtg ctg ggg gct ccc ctg gtg 401

59 /346

Ala Pro Leu Thr Ala Ile Ala Leu Leu Val Leu Gly Ala Pro Leu Val
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 ctg gcc ggc gag gac tgc ctg tgg tac ctg gac cgg aat ggc tcc tgg 449
 Leu Ala Gly Glu Asp Cys Leu Trp Tyr Leu Asp Arg Asn Gly Ser Trp
 5 30 35 40
 cat ccg ggg ttt aac tgc gag ttc ttc acc ttc tgc tgc ggg acc tgc 497
 His Pro Gly Phe Asn Cys Glu Phe Phe Thr Phe Cys Cys Gly Thr Cys
 45 50 55
 tac cat cgg tac tgc tgc agg gac ctg acc ttg ctt atc acc gag agg 545
 10 Tyr His Arg Tyr Cys Cys Arg Asp Leu Thr Leu Leu Ile Thr Glu Arg
 60 65 70
 cag cag aag cac tgc ctg gcc ttc agc ccc aag acc ata gca ggc atc 593
 Gln Gln Lys His Cys Leu Ala Phe Ser Pro Lys Thr Ile Ala Gly Ile
 75 80 85
 15 gcc tca gct gtg atc ctc ttt gtt gct gtg gtt gcc acc acc atc tgc 641
 Ala Ser Ala Val Ile Leu Phe Val Ala Val Val Ala Thr Thr Ile Cys
 90 95 100 105
 tgc ttc ctc tgt tcc tgt tgc tac ctg tac cgc cgg cgc cag cag ctc 689
 Cys Phe Leu Cys Ser Cys Cys Tyr Leu Tyr Arg Arg Arg Gln Gln Leu
 20 110 115 120
 cag agc cca ttt gaa ggc cag gag att cca atg aca ggc atc cca gtg 737
 Gln Ser Pro Phe Glu Gly Gln Glu Ile Pro Met Thr Gly Ile Pro Val
 125 130 135
 cag cca gta tac cca tac ccc cag gac ccc aaa gct ggc cct gca ccc 785
 25 Gln Pro Val Tyr Pro Tyr Pro Gln Asp Pro Lys Ala Gly Pro Ala Pro

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140 145 150
cca cag cct ggc ttc ata tac cca cct agt ggt cct gct ccc caa tat 833
Pro Gln Pro Gly Phe Ile Tyr Pro Pro Ser Gly Pro Ala Pro Gln Tyr
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65 /346

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66 /346

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	Ala Ala Ala Gly Ser Ser Val Val Ser Glu Ser Ala Val Ser Trp Glu			
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70 /346

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72 /346

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73 /346

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75 /346

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 5 Val Ala Leu Gly Thr Val Ala Trp Arg Arg Ala Trp Pro Arg Arg Arg
 35 40 45
 Arg Arg Leu Gln Gln Val Gly Thr Val Ala Lys Leu Trp Ile Tyr Pro
 50 55 60
 Val Lys Ser Cys Lys Gly Val Pro Val Ser Glu Ala Glu Cys Thr Ala
 10 65 70 75 80
 Met Gly Leu Arg Ser Gly Asn Leu Arg Asp Arg Phe Trp Leu Val Ile
 85 90 95
 Lys Glu Asp Gly His Met Val Thr Ala Arg Gln Glu Pro Arg Leu Val
 100 105 110
 15 Leu Ile Ser Ile Ile Tyr Glu Asn Asn Cys Leu Ile Phe Arg Ala Pro
 115 120 125
 Asp Met Asp Gln Leu Val Leu Pro Ser Lys Gln Pro Ser Ser Asn Lys
 130 135 140
 Leu His Asn Cys Arg Ile Phe Gly Leu Asp Ile Lys Gly Arg Asp Cys
 20 145 150 155 160
 Gly Asn Glu Ala Ala Lys Trp Phe Thr Asn Phe Leu Lys Thr Glu Ala
 165 170 175
 Tyr Arg Leu Val Gln Phe Glu Thr Asn Met Lys Gly Arg Thr Ser Arg
 180 185 190
 25 Lys Leu Leu Pro Thr Leu Asp Gln Asn Phe Gln Val Ala Tyr Pro Asp

76 /346

195 200 205
Tyr Cys Pro Leu Leu Ile Met Thr Asp Ala Ser Leu Val Asp Leu Asn
210 215 220
Thr Arg Met Glu Lys Lys Met Lys Met Glu Asn Phe Arg Pro Asn Ile
5 225 230 235 240
Val Val Thr Gly Cys Asp Ala Phe Glu Glu Asp Thr Trp Asp Glu Leu
245 250 255
Leu Ile Gly Ser Val Glu Val Lys Lys Val Met Ala Cys Pro Arg Cys
260 265 270
10 Ile Leu Thr Thr Val Asp Pro Asp Thr Gly Val Ile Asp Arg Lys Gln
275 280 285
Pro Leu Asp Thr Leu Lys Ser Tyr Arg Leu Cys Asp Pro Ser Glu Arg
290 295 300
Glu Leu Tyr Lys Leu Ser Pro Leu Phe Gly Ile Tyr Tyr Ser Val Glu
15 305 310 315 320
Lys Ile Gly Ser Leu Arg Val Gly Asp Pro Val Tyr Arg Met Val
325 330 335

<210> 32
20 <211> 208
<212> PRT
<213> Homo sapiens
<400> 32
Met Glu Leu Arg Ala Ala Leu Val Leu Val Val Leu Leu Ile Ala Gly
25 .1 5 10 15

77 / 346

Gly Leu Phe Met Phe Thr Tyr Lys Ser Thr Gln Phe Asn Val Glu Gly
 20 25 30
 Phe Ala Leu Val Leu Gly Ala Ser Phe Ile Gly Gly Ile Arg Trp Thr
 35 40 45
 5 Leu Thr Gln Met Leu Leu Gln Lys Ala Glu Leu Gly Leu Gln Asn Pro
 50 55 60
 Ile Asp Thr Met Phe His Leu Gln Pro Leu Met Phe Leu Gly Leu Phe
 65 70 75 80
 Pro Leu Phe Ala Val Phe Glu Gly Leu His Leu Ser Thr Ser Glu Lys
 10 85 90 95
 Ile Phe Arg Phe Gln Asp Thr Gly Leu Leu Leu Arg Val Leu Gly Ser
 100 105 110
 Leu Phe Leu Gly Gly Ile Leu Ala Phe Gly Leu Gly Phe Ser Glu Phe
 115 120 125
 15 Leu Leu Val Ser Arg Thr Ser Ser Leu Thr Leu Ser Ile Ala Gly Ile
 130 135 140
 Phe Lys Glu Val Cys Thr Leu Leu Leu Ala Ala His Leu Leu Gly Asp
 145 150 155 160
 Gln Ile Ser Leu Leu Asn Trp Leu Gly Phe Ala Leu Cys Leu Ser Gly
 20 165 170 175
 Ile Ser Leu His Val Ala Leu Lys Ala Leu His Ser Arg Gly Asn Pro
 180 185 190
 Glu Ser Leu Pro Glu Ala Ser Val Phe Cys Ser Ser Pro Cys Asp Ser
 195 200 205

25

78 /346

<210> 33

<211> 406

<212> PRT

<213> Homo sapiens

5 <400> 33

Met Ala Ala Gly Ala Gly Ala Gly Ser Ala Pro Arg Trp Leu Arg Ala

1 5 10 15

Leu Ser Glu Pro Leu Ser Ala Ala Gln Leu Arg Arg Leu Glu Glu His

20 25 30

10 Arg Tyr Ser Ala Ala Gly Val Ser Leu Leu Glu Pro Pro Leu Gln Leu

35 40 45

Tyr Trp Thr Trp Leu Leu Gln Trp Ile Pro Leu Trp Met Ala Pro Asn

50 55 60

Ser Ile Thr Leu Leu Gly Leu Ala Val Asn Val Val Thr Thr Leu Val

15 65 70 75 80

Leu Ile Ser Tyr Cys Pro Thr Ala Thr Glu Glu Ala Pro Tyr Trp Thr

85 90 95

Tyr Leu Leu Cys Ala Leu Gly Leu Phe Ile Tyr Gln Ser Leu Asp Ala

100 105 110

20 Ile Asp Gly Lys Gln Ala Arg Arg Thr Asn Ser Cys Ser Pro Leu Gly

115 120 125

Glu Leu Phe Asp His Gly Cys Asp Ser Leu Ser Thr Val Phe Met Ala

130 135 140

Val Gly Ala Ser Ile Ala Ala Arg Leu Gly Thr Tyr Pro Asp Trp Phe

25 145 150 155 160

79 /346

	Phe	Phe	Cys	Ser	Phe	Ile	Gly	Met	Phe	Val	Phe	Tyr	Cys	Ala	His	Trp
					165					170					175	
	Gln	Thr	Tyr	Val	Ser	Gly	Met	Leu	Arg	Phe	Gly	Lys	Val	Asp	Val	Thr
					180					185					190	
5	Glu	Ile	Gln	Ile	Ala	Leu	Val	Ile	Val	Phe	Val	Leu	Ser	Ala	Phe	Gly
					195					200					205	
	Gly	Ala	Thr	Met	Trp	Asp	Tyr	Thr	Ile	Pro	Ile	Leu	Glu	Ile	Lys	Leu
					210					215					220	
	Lys	Ile	Leu	Pro	Val	Leu	Gly	Phe	Leu	Gly	Gly	Val	Ile	Phe	Ser	Cys
10		225				230					235				240	
	Ser	Asn	Tyr	Phe	His	Val	Ile	Leu	His	Gly	Gly	Val	Gly	Lys	Asn	Gly
					245					250					255	
	Ser	Thr	Ile	Ala	Gly	Thr	Ser	Val	Leu	Ser	Pro	Gly	Leu	His	Ile	Gly
					260					265					270	
15	Leu	Ile	Ile	Ile	Leu	Ala	Ile	Met	Ile	Tyr	Lys	Lys	Ser	Ala	Thr	Asp
					275					280					285	
	Val	Phe	Glu	Lys	His	Pro	Cys	Leu	Tyr	Ile	Leu	Met	Phe	Gly	Cys	Val
					290					295					300	
	Phe	Ala	Lys	Val	Ser	Gln	Lys	Leu	Val	Val	Ala	His	Met	Thr	Lys	Ser
20		305				310					315				320	
	Glu	Leu	Tyr	Leu	Gln	Asp	Thr	Val	Phe	Leu	Gly	Pro	Gly	Leu	Leu	Phe
					325						330				335	
	Leu	Asp	Gln	Tyr	Phe	Asn	Asn	Phe	Ile	Asp	Glu	Tyr	Val	Val	Leu	Trp
					340					345					350	
25	Met	Ala	Met	Val	Ile	Ser	Ser	Phe	Asp	Met	Val	Ile	Tyr	Phe	Ser	Ala

80 /346

355 360 365
 Leu Cys Leu Gln Ile Ser Arg His Leu His Leu Asn Ile Phe Lys Thr
 370 375 380
 Ala Cys His Gln Ala Pro Glu Gln Val Gln Val Leu Ser Ser Lys Ser
 5 385 390 395 400
 His Gln Asn Asn Met Asp
 405
 <210> 34
 10 <211> 618
 <212> PRT
 <213> Homo sapiens
 <400> 34
 Met Glu Val Lys Asn Phe Ala Val Trp Asp Tyr Val Val Phe Ala Ala
 15 1 5 10 15
 Leu Phe Phe Ile Ser Ser Gly Ile Gly Val Phe Phe Ala Ile Lys Glu
 20 25 30
 Arg Lys Lys Ala Thr Ser Arg Glu Phe Leu Val Gly Gly Arg Gln Met
 35 40 45
 20 Ser Phe Gly Pro Val Gly Leu Ser Leu Thr Ala Ser Phe Met Ser Ala
 50 55 60
 Val Thr Val Leu Gly Thr Pro Ser Glu Val Tyr Arg Phe Gly Ala Ser
 65 70 75 80
 Phe Leu Val Phe Phe Ile Ala Tyr Leu Phe Val Ile Leu Leu Thr Ser
 25 85 90 95

81 /346

Glu Leu Phe Leu Pro Val Phe Tyr Arg Ser Gly Ile Thr Ser Thr Tyr
 100 105 110
 Glu Tyr Leu Gln Leu Arg Phe Asn Lys Pro Val Arg Tyr Ala Ala Thr
 115 120 125
 5 Val Ile Tyr Ile Val Gln Thr Ile Leu Tyr Thr Gly Val Val Val Tyr
 130 135 140
 Ala Pro Ala Leu Ala Leu Asn Gln Val Thr Gly Phe Asp Leu Trp Gly
 145 150 155 160
 Ser Val Phe Ala Thr Gly Ile Val Cys Thr Phe Tyr Cys Thr Leu Gly
 10 165 170 175
 Gly Leu Lys Ala Val Val Trp Thr Asp Ala Phe Gln Met Val Val Met
 180 185 190
 Ile Val Gly Phe Leu Thr Val Leu Ile Gln Gly Ser Thr His Ala Gly
 195 200 205
 15 Gly Phe His Asn Val Leu Glu Gln Ser Thr Asn Gly Ser Arg Leu His
 210 215 220
 Ile Phe Asp Phe Asp Val Asp Pro Leu Arg Arg His Thr Phe Trp Thr
 225 230 235 240
 Ile Thr Val Gly Gly Thr Phe Thr Trp Leu Gly Ile Tyr Gly Val Asn
 20 245 250 255
 Gln Ser Thr Ile Gln Arg Cys Ile Ser Cys Lys Thr Glu Lys His Ala
 260 265 270
 Lys Leu Ala Leu Tyr Phe Asn Leu Leu Gly Leu Trp Ile Ile Leu Val
 275 280 285
 25 Cys Ala Val Phe Ser Gly Leu Ile Met Tyr Ser His Phe Lys Asp Cys

82 /346

	290	295	300	
	Asp Pro Trp Thr Ser Gly Ile Ile Ser Ala Pro Asp Gln Leu Met Pro			
	305	310	315	320
	Tyr Phe Val Met Glu Ile Phe Ala Thr Met Pro Gly Leu Pro Gly Leu			
5	325	330	335	
	Phe Val Ala Cys Ala Phe Ser Gly Thr Leu Ser Thr Val Ala Ser Ser			
	340	345	350	
	Ile Asn Ala Leu Ala Thr Val Thr Phe Glu Asp Phe Val Lys Ser Cys			
	355	360	365	
10	Phe Pro His Leu Ser Asp Lys Leu Ser Thr Trp Ile Ser Lys Gly Leu			
	370	375	380	
	Cys Leu Leu Phe Gly Val Met Cys Thr Ser Met Ala Val Ala Ala Ser			
	385	390	395	400
	Val Met Gly Gly Val Val Gln Ala Ser Leu Ser Ile His Gly Met Cys			
15	405	410	415	
	Gly Gly Pro Met Leu Gly Leu Phe Ser Leu Gly Ile Val Phe Pro Phe			
	420	425	430	
	Val Asn Trp Lys Gly Ala Leu Gly Gly Leu Leu Thr Gly Ile Thr Leu			
	435	440	445	
20	Ser Phe Trp Val Ala Ile Gly Ala Phe Ile Tyr Pro Ala Pro Ala Ser			
	450	455	460	
	Lys Thr Trp Pro Leu Pro Leu Ser Thr Asp Gln Cys Ile Lys Ser Asn			
	465	470	475	480
	Val Thr Ala Thr Gly Pro Pro Val Leu Ser Ser Arg Pro Gly Ile Ala			
25	485	490	495	

83 /346

Asp Thr Trp Tyr Ser Ile Ser Tyr Leu Tyr Tyr Ser Ala Val Gly Cys
 500 505 510
 Leu Gly Cys Ile Val Ala Gly Val Ile Ile Ser Leu Ile Thr Gly Arg
 515 520 525
 5 Gln Arg Gly Glu Asp Ile Gln Pro Leu Leu Ile Arg Pro Val Cys Asn
 530 535 540
 Leu Phe Cys Phe Trp Ser Lys Lys Tyr Lys Thr Leu Cys Trp Cys Gly
 545 550 555 560
 Val Gln His Asp Ser Gly Thr Glu Gln Glu Asn Leu Glu Asn Gly Ser
 10 565 570 575
 Ala Arg Lys Gln Gly Ala Glu Ser Val Leu Gln Asn Gly Leu Arg Arg
 580 585 590
 Glu Ser Leu Val His Val Pro Gly Tyr Asp Pro Lys Asp Lys Ser Tyr
 595 600 605
 15 Asn Asn Met Ala Phe Glu Thr Thr His Phe
 610 615

 <210> 35
 <211> 208
 20 <212> PRT
 <213> Homo sapiens
 <400> 35

 Met Gly Leu Gly Ala Arg Gly Ala Trp Ala Ala Leu Leu Leu Gly Thr
 1 5 10 15
 25 Leu Gln Val Leu Ala Leu Leu Gly Ala Ala His Glu Ser Ala Ala Met

84 /346

	20	25	30
	Ala Ala Ser Ala Asn Ile Glu Asn Ser Gly Leu Pro His Asn Ser Ser		
	35	40	45
	Ala Asn Ser Thr Glu Thr Leu Gln His Val Pro Ser Asp His Thr Asn		
5	50	55	60
	Glu Thr Ser Asn Ser Thr Val Lys Pro Pro Thr Ser Val Ala Ser Asp		
	65	70	75 80
	Ser Ser Asn Thr Thr Val Thr Thr Met Lys Pro Thr Ala Ala Ser Asn		
	85	90	95
10	Thr Thr Thr Pro Gly Met Val Ser Thr Asn Met Thr Ser Thr Thr Leu		
	100	105	110
	Lys Ser Thr Pro Lys Thr Thr Ser Val Ser Gln Asn Thr Ser Gln Ile		
	115	120	125
	Ser Thr Ser Thr Met Thr Val Thr His Asn Ser Ser Val Thr Ser Ala		
15	130	135	140
	Ala Ser Ser Val Thr Ile Thr Thr Thr Met His Ser Glu Ala Lys Lys		
	145	150	155 160
	Gly Ser Lys Phe Asp Thr Gly Ser Phe Val Gly Gly Ile Val Leu Thr		
	165	170	175
20	Leu Gly Val Leu Ser Ile Leu Tyr Ile Gly Cys Lys Met Tyr Tyr Ser		
	180	185	190
	Arg Arg Gly Ile Arg Tyr Arg Thr Ile Asp Glu His Asp Ala Ile Ile		
	195	200	205
25	<210> 36		

85 / 346

<211> 502

<212> PRT

<213> Homo sapiens

<400> 36

5 Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
1 5 10 15
Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
20 25 30
Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
10 35 40 45
Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60
Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
65 70 75 80
15 Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95
Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
100 105 110
Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
20 115 120 125
Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
130 135 140
Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
145 150 155 160
25 Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala

86 / 346

	165	170	175
	Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu		
	180	185	190
	Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met		
5	195	200	205
	Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu		
	210	215	220
	Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr		
	225	230	235 240
10	Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr		
	245	250	255
	Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro		
	260	265	270
	Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly		
15	275	280	285
	Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val		
	290	295	300
	Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys		
	305	310	315 320
20	Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val		
	325	330	335
	Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr		
	340	345	350
	Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp		
25	355	360	365

87 /346

Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr
 370 375 380
 Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val
 385 390 395 400
 5 Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser
 405 410 415
 Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser
 420 425 430
 Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe
 10 435 440 445
 Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro
 450 455 460
 Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu
 465 470 475 480
 15 His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His
 485 490 495
 Asp Gly Cys Cys Ser Leu
 500

20 <210> 37

<211> 336

<212> PRT

<213> Homo sapiens

<400> 37

25 Met Arg Ala Pro Ser Met Asp Arg Ala Ala Val Ala Arg Val Gly Ala

88 /346

	1		5		10		15									
	Val	Ala	Ser	Ala	Ser	Val	Cys	Ala	Leu	Val	Ala	Gly	Val	Val	Leu	Ala
				20				25							30	
	Gln	Tyr	Ile	Phe	Thr	Leu	Lys	Arg	Lys	Thr	Gly	Arg	Lys	Thr	Lys	Ile
5			35					40							45	
	Ile	Glu	Met	Met	Pro	Glu	Phe	Gln	Lys	Ser	Ser	Val	Arg	Ile	Lys	Asn
			50					55							60	
	Pro	Thr	Arg	Val	Glu	Glu	Ile	Ile	Cys	Gly	Leu	Ile	Lys	Gly	Gly	Ala
		65					70					75			80	
10	Ala	Lys	Leu	Gln	Ile	Ile	Thr	Asp	Phe	Asp	Met	Thr	Leu	Ser	Arg	Phe
							85					90			95	
	Ser	Tyr	Lys	Gly	Lys	Arg	Cys	Pro	Thr	Cys	His	Asn	Ile	Ile	Asp	Asn
							100					105			110	
	Cys	Lys	Leu	Val	Thr	Asp	Glu	Cys	Arg	Lys	Lys	Leu	Leu	Gln	Leu	Lys
15			115					120							125	
	Glu	Lys	Tyr	Tyr	Ala	Ile	Glu	Val	Asp	Pro	Val	Leu	Thr	Val	Glu	Glu
			130					135							140	
	Lys	Tyr	Pro	Tyr	Met	Val	Glu	Trp	Tyr	Thr	Lys	Ser	His	Gly	Leu	Leu
		145					150					155			160	
20	Val	Gln	Gln	Ala	Leu	Pro	Lys	Ala	Lys	Leu	Lys	Glu	Ile	Val	Ala	Glu
							165					170			175	
	Ser	Asp	Val	Met	Leu	Lys	Glu	Gly	Tyr	Glu	Asn	Phe	Phe	Asp	Lys	Leu
							180					185			190	
	Gln	Gln	His	Ser	Ile	Pro	Val	Phe	Ile	Phe	Ser	Ala	Gly	Ile	Gly	Asp
25							195					200			205	

89 /346

Val Leu Glu Glu Val Ile Arg Gln Ala Gly Val Tyr His Pro Asn Val
210 215 220
Lys Val Val Ser Asn Phe Met Asp Phe Asp Glu Thr Gly Val Leu Lys
225 230 235 240
5 Gly Phe Lys Gly Glu Leu Ile His Val Phe Asn Lys His Asp Gly Ala
245 250 255
Leu Arg Asn Thr Glu Tyr Phe Asn Gln Leu Lys Asp Asn Ser Asn Ile
260 265 270
Ile Leu Leu Gly Asp Ser Gln Gly Asp Leu Arg Met Ala Asp Gly Val
10 275 280 285
Ala Asn Val Glu His Ile Leu Lys Ile Gly Tyr Leu Asn Asp Arg Val
290 295 300
Asp Glu Leu Leu Glu Lys Tyr Met Asp Ser Tyr Asp Ile Val Leu Val
305 310 315 320
15 Gln Asp Glu Ser Leu Glu Val Ala Asn Ser Ile Leu Gln Lys Ile Leu
325 330 335

<210> 38
<211> 340
20 <212> PRT
<213> Homo sapiens
<400> 38

Met Glu Pro Gly Arg Thr Gln Ile Lys Leu Asp Pro Arg Tyr Thr Ala
1 5 10 15
25 Asp Leu Leu Glu Val Leu Lys Thr Asn Tyr Gly Ile Pro Ser Ala Cys

90 /346

	20	25	30
	Phe Ser Gln Pro Pro Thr Ala Ala Gln Leu Leu Arg Ala Leu Gly Pro		
	35	40	45
	Val Glu Leu Ala Leu Thr Ser Ile Leu Thr Leu Leu Ala Leu Gly Ser		
5	50	55	60
	Ile Ala Ile Phe Leu Glu Asp Ala Val Tyr Leu Tyr Lys Asn Thr Leu		
	65	70	75 80
	Cys Pro Ile Lys Arg Arg Thr Leu Leu Trp Lys Ser Ser Ala Pro Thr		
	85	90	95
10	Val Val Ser Val Leu Cys Cys Phe Gly Leu Trp Ile Pro Arg Ser Leu		
	100	105	110
	Val Leu Val Glu Met Thr Ile Thr Ser Phe Tyr Ala Val Cys Phe Tyr		
	115	120	125
	Leu Leu Met Leu Val Met Val Glu Gly Phe Gly Gly Lys Glu Ala Val		
15	130	135	140
	Leu Arg Thr Leu Arg Asp Thr Pro Met Met Val His Thr Gly Pro Cys		
	145	150	155 160
	Cys Cys Cys Cys Pro Cys Cys Pro Arg Leu Leu Leu Thr Arg Lys Lys		
	165	170	175
20	Leu Gln Leu Leu Met Leu Gly Pro Phe Gln Tyr Ala Phe Leu Lys Ile		
	180	185	190
	Thr Leu Thr Leu Val Gly Leu Phe Leu Ile Pro Asp Gly Ile Tyr Asp		
	195	200	205
	Pro Ala Asp Ile Ser Glu Gly Ser Thr Ala Leu Trp Ile Asn Thr Phe		
25	210	215	220

91 /346

Leu Gly Val Ser Thr Leu Leu Ala Leu Trp Thr Leu Gly Ile Ile Ser
 225 230 235 240
 Arg Gln Ala Arg Leu His Leu Gly Glu Gln Asn Met Gly Ala Lys Phe
 245 250 255
 5 Ala Leu Phe Gln Val Leu Leu Ile Leu Thr Ala Leu Gln Pro Ser Ile
 260 265 270
 Phe Ser Val Leu Ala Asn Gly Gly Gln Ile Ala Cys Ser Pro Pro Tyr
 275 280 285
 Ser Ser Lys Thr Arg Ser Gln Val Met Asn Cys His Leu Leu Ile Leu
 10 290 295 300
 Glu Thr Phe Leu Met Thr Val Leu Thr Arg Met Tyr Tyr Arg Arg Lys
 305 310 315 320
 Asp His Lys Val Gly Tyr Glu Thr Phe Ser Ser Pro Asp Leu Asp Leu
 325 330 335
 15 Asn Leu Lys Ala
 340

 <210> 39
 <211> 223
 20 <212> PRT

 <213> Homo sapiens

 <400> 39

 Met Leu Trp Arg Gln Leu Ile Tyr Trp Gln Leu Leu Ala Leu Phe Phe
 1 5 10 15
 25 Leu Pro Phe Cys Leu Cys Gln Asp Glu Tyr Met Glu Val Ser Gly Arg

92 /346

	20	25	30
	Thr Asn Lys Val Val Ala Arg Ile Val Gln Ser His Gln Gln Thr Gly		
	35	40	45
	Arg Ser Gly Ser Arg Arg Glu Lys Val Arg Glu Arg Ser His Pro Lys		
5	50	55	60
	Thr Gly Thr Val Asp Asn Asn Thr Ser Thr Asp Leu Lys Ser Leu Arg		
	65	70	75 80
	Pro Asp Glu Leu Pro His Pro Glu Val Asp Asp Leu Ala Gln Ile Thr		
	85	90	95
10	Thr Phe Trp Gly Gln Ser Pro Gln Thr Gly Gly Leu Pro Pro Asp Cys		
	100	105	110
	Ser Lys Cys Cys His Gly Asp Tyr Ser Phe Arg Gly Tyr Gln Gly Pro		
	115	120	125
	Pro Gly Pro Pro Gly Pro Pro Gly Ile Pro Gly Asn His Gly Asn Asn		
15	130	135	140
	Gly Asn Asn Gly Ala Thr Gly His Glu Gly Ala Lys Gly Glu Lys Gly		
	145	150	155 160
	Asp Lys Gly Asp Leu Gly Pro Arg Gly Glu Arg Gly Gln His Gly Pro		
	165	170	175
20	Lys Gly Glu Lys Gly Tyr Pro Gly Ile Pro Pro Glu Leu Gln Ile Ala		
	180	185	190
	Phe Met Ala Ser Leu Ala Thr His Phe Ser Asn Gln Asn Ser Gly Ile		
	195	200	205
	Ile Phe Ser Ser Val Glu Thr Asn Ile Gly Asn Phe Leu Met Ser		
25	210	215	220

93 /346

<210> 40
<211> 309
<212> PRT
5 <213> Homo sapiens
<400> 40
Met Ala Thr Leu Ser Val Ile Gly Ser Ser Ser Leu Ile Ala Tyr Ala
1 5 10 15
Val Phe His Asn Ile Gln Lys Ser Pro Glu Ile Arg Pro Leu Phe Tyr
10 20 25 30
Leu Ser Phe Cys Asp Leu Leu Leu Gly Leu Cys Trp Leu Thr Glu Thr
35 40 45
Leu Leu Tyr Gly Ala Ser Val Ala Asn Lys Asp Ile Ile Cys Tyr Asn
50 55 60
15 Leu Gln Ala Val Gly Gln Ile Phe Tyr Ile Ser Ser Phe Leu Tyr Thr
65 70 75 80
Val Asn Tyr Ile Trp Tyr Leu Tyr Thr Glu Leu Arg Met Lys His Thr
85 90 95
Gln Ser Gly Gln Ser Thr Ser Pro Leu Val Ile Asp Tyr Thr Cys Arg
20 100 105 110
Val Cys Gln Met Ala Phe Val Phe Ser Arg Cys Ile Leu Met His Ser
115 120 125
Pro Pro Ser Ala Met Ala Glu Leu Pro Pro Ser Ala Asn Thr Ser Val
130 135 140
25 Cys Ser Thr Leu Tyr Phe Tyr Gly Ile Ala Ile Phe Leu Gly Ser Phe

94 /346

145 150 155 160
Val Leu Ser Leu Leu Thr Ile Met Val Leu Leu Ile Arg Ala Gln Thr
165 170 175
Leu Tyr Lys Lys Phe Val Lys Ser Thr Gly Phe Leu Gly Ser Glu Gln
5 180 185 190
Trp Ala Val Ile His Ile Val Asp Gln Arg Val Arg Phe Tyr Pro Val
195 200 205
Ala Phe Phe Cys Cys Trp Gly Pro Ala Val Ile Leu Met Ile Ile Lys
210 215 220
10 Leu Thr Lys Pro Gln Asp Thr Lys Leu His Met Ala Leu Tyr Val Leu
225 230 235 240
Gln Ala Leu Thr Ala Thr Ser Gln Gly Leu Leu Asn Cys Gly Val Tyr
245 250 255
Gly Trp Thr Gln His Lys Phe His Gln Leu Lys Gln Glu Ala Arg Arg
15 260 265 270
Asp Ala Asp Thr Gln Thr Pro Leu Leu Cys Ser Gln Lys Arg Phe Tyr
275 280 285
Ser Arg Gly Leu Asn Ser Leu Glu Ser Thr Leu Thr Phe Pro Ala Ser
290 295 300
20 Thr Ser Thr Ile Phe
305

<210> 41

<211> 1008

25 <212> DNA

95 / 346

<213> Homo sapiens

<400> 41

atgggcgctt ccagctcctc cgcgctggcc cgcctcggcc tcccagcccg gccctggccc 60
aggtggctcg gggtcgccgc gctaggactg gccgccgtgg ccctggggac tgtcgcttg 120
5 cgccgcgcat ggcccaggcg gcgccggcgg ctgcagcagg tgggcaccgt ggcgaagctc 180
tggatctacc cggtgaaatc ctgcaaaggg gtgccggtga gcgaggctga gtgcacggcc 240
atggggctgc gcagcggcaa cctgcgggac aggttttggc tggtgattaa ggaagatgga 300
cacatggtca ctgcccga ca ggagcctcgc ctctgtctca tctccatcat ttatgagaat 360
aactgcctga tcttcagggc tccagacatg gaccagctgg ttttgcctag caagcagcct 420
10 tcctcaaaca aactccacaa ctgcaggata tttggccttg acattaaagg cagagactgt 480
ggcaatgagg cagctaagtg gttcaccaac ttcttgaaaa ctgaagcgta tagattgggtt 540
caatttgaga caaacatgaa gggaagaaca tcaagaaaac ttctccccac tcttgatcag 600
aatttccagg tggcctaccc agactactgc ccgctcctga tcatgacaga tgcctccctg 660
gtagatttga ataccaggat ggagaagaaa atgaaaatgg agaatttcag gccaaatatt 720
15 gtggtgaccg gctgtgatgc ttttgaggag gatacctggg atgaactcct aattggtagt 780
gtagaagtga aaaaggtaat ggcattgccc aggtgtattt tgacaacggt ggaccagac 840
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<211> 627

<212> DNA

<213> Homo sapiens

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<400> 42

96 /346

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15 <211> 1221

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<213> Homo sapiens)

<400> 43

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97 / 346

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15

<210> 44

<211> 1857

<212> DNA

<213> Homo sapiens

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<400> 44

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 25 ttcttagtct tcttcattgc ttacctattt gtcatcctct taacatcaga gctctttctc 300

98 / 346

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25 ggggctgaat ctgtcttaca gaacggactc agaagagaaa gcctggtaca tgttccaggc 1800

99 / 346

tatgatccta aggacaaaag ctacaacaat atggcatttg agactacca tttctaa 1857

<210> 45

<211> 627

5 <212> DNA

<213> Homo sapiens

<400> 45

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10 tctgggcttc cacacaactc cagtgtctaac tcaacagaga ctctccaaca tgtgccttct 180
gaccatacaa atgaaacttc caacagtact gtgaaaccac caacttcagt tgcctcagac 240
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ggatcaaaat ttgatactgg gagctttgtt ggtggtattg tattaacgct gggagtttta 540
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<211> 1509

<212> DNA

<213> Homo sapiens

<400> 46

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100/346

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101/346

<210> 47

<211> 1011

<212> DNA

5 <213> Homo sapiens

<400> 47

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aagacggggc ggaagaccaa gatcatcgag atgatgccag aattccagaa aagttcagtt 180
10 cgaatcaaga accctacaag agtagaagaa attatctgtg gtcttatcaa aggaggagct 240
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aatgatagag tggatgagct tttagaaaag tacatggact cttatgatat tgttttagta 960
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25 <210> 48

102/346

<211> 1023

<212> DNA

<213> Homo sapiens

<400> 48

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<210> 49

25 <211> 672

103/346

<212> DNA

<213> Homo sapiens

<400> 49

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ggctacccgg ggattccacc agaacttcag attgcattca tggcttctct ggcaaccac 600
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15 ttgatgtcat ga 672

<210> 50

<211> 930

<212> DNA

20 <213> Homo sapiens

<400> 50

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25 atctgctata acctacaagc agttggacag atattctaca tttcctcatt tctctacacc 240

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gtcaattaca tctggtatTT gtacacagag ctgaggatga aacacacca gaggggacag 300
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15 <211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

20 <222> (255)..(1262)

<400> 51

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105/346

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 Met Gly Ala Ser Ser Ser Ser Ala Leu Ala Arg Leu
 1 5 10
 ggc ctc cca gcc cgg ccc tgg ccc agg tgg ctc ggg gtc gcc gcg cta 338
 5 Gly Leu Pro Ala Arg Pro Trp Pro Arg Trp Leu Gly Val Ala Ala Leu
 15 20 25
 gga ctg gcc gcc gtg gcc ctg ggg act gtc gcc tgg cgc cgc gca tgg 386
 Gly Leu Ala Ala Val Ala Leu Gly Thr Val Ala Trp Arg Arg Ala Trp
 30 35 40
 10 ccc agg cgg cgc cgg cgg ctg cag cag gtg ggc acc gtg gcg aag ctc 434
 Pro Arg Arg Arg Arg Arg Leu Gln Gln Val Gly Thr Val Ala Lys Leu
 45 50 55 60
 tgg atc tac ccg gtg aaa tcc tgc aaa ggg gtg ccg gtg agc gag gct 482
 Trp Ile Tyr Pro Val Lys Ser Cys Lys Gly Val Pro Val Ser Glu Ala
 15 65 70 75
 gag tgc acg gcc atg ggg ctg cgc agc ggc aac ctg cgg gac agg ttt 530
 Glu Cys Thr Ala Met Gly Leu Arg Ser Gly Asn Leu Arg Asp Arg Phe
 80 85 90
 tgg ctg gtg att aag gaa gat gga cac atg gtc act gcc cga cag gag 578
 20 Trp Leu Val Ile Lys Glu Asp Gly His Met Val Thr Ala Arg Gln Glu
 95 100 105
 cct cgc ctc gtg ctc atc tcc atc att tat gag aat aac tgc ctg atc 626
 Pro Arg Leu Val Leu Ile Ser Ile Ile Tyr Glu Asn Asn Cys Leu Ile
 110 115 120
 25 ttc agg gct cca gac atg gac cag ctg gtt ttg cct agc aag cag cct 674

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Phe Arg Ala Pro Asp Met Asp Gln Leu Val Leu Pro Ser Lys Gln Pro
 125 130 135 140
 tcc tca aac aaa ctc cac aac tgc agg ata ttt ggc ctt gac att aaa 722
 Ser Ser Asn Lys Leu His Asn Cys Arg Ile Phe Gly Leu Asp Ile Lys
 5 145 150 155
 ggc aga gac tgt ggc aat gag gca gct aag tgg ttc acc aac ttc ttg 770
 Gly Arg Asp Cys Gly Asn Glu Ala Ala Lys Trp Phe Thr Asn Phe Leu
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 aaa act gaa gcg tat aga ttg gtt caa ttt gag aca aac atg aag gga 818
 10 Lys Thr Glu Ala Tyr Arg Leu Val Gln Phe Glu Thr Asn Met Lys Gly
 175 180 185
 aga aca tca aga aaa ctt ctc ccc act ctt gat cag aat ttc cag gtg 866
 Arg Thr Ser Arg Lys Leu Leu Pro Thr Leu Asp Gln Asn Phe Gln Val
 190 195 200
 15 gcc tac cca gac tac tgc ccg ctc ctg atc atg aca gat gcc tcc ctg 914
 Ala Tyr Pro Asp Tyr Cys Pro Leu Leu Ile Met Thr Asp Ala Ser Leu
 205 210 215 220
 gta gat ttg aat acc agg atg gag aag aaa atg aaa atg gag aat ttc 962
 Val Asp Leu Asn Thr Arg Met Glu Lys Lys Met Lys Met Glu Asn Phe
 20 225 230 235
 agg cca aat att gtg gtg acc ggc tgt gat gct ttt gag gag gat acc 1010
 Arg Pro Asn Ile Val Val Thr Gly Cys Asp Ala Phe Glu Glu Asp Thr
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 tgg gat gaa ctc cta att ggt agt gta gaa gtg aaa aag gta atg gca 1058
 25 Trp Asp Glu Leu Leu Ile Gly Ser Val Glu Val Lys Lys Val Met Ala

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255 260 265
 tgc ccc agg tgt att ttg aca acg gtg gac cca gac act gga gtc ata 1106
 Cys Pro Arg Cys Ile Leu Thr Thr Val Asp Pro Asp Thr Gly Val Ile
 270 275 280
 5 gac agg aaa cag cca ctg gac acc ctg aag agc tac cgc ctg tgt gat 1154
 Asp Arg Lys Gln Pro Leu Asp Thr Leu Lys Ser Tyr Arg Leu Cys Asp
 285 290 295 300
 cct tct gag agg gaa ttg tac aag ttg tct cca ctt ttt ggg atc tat 1202
 Pro Ser Glu Arg Glu Leu Tyr Lys Leu Ser Pro Leu Phe Gly Ile Tyr
 10 305 310 315
 tat tca gtg gaa aaa att gga agc ctg aga gtt ggt gac cct gtg tat 1250
 Tyr Ser Val Glu Lys Ile Gly Ser Leu Arg Val Gly Asp Pro Val Tyr
 320 325 330
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 25 <211> 1749

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

5 <222> (159)..(785)

<400> 52

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 gaggactctc cctggggctc tgctgatggt tccgaatc atg gag ctg cgc gcg gca 176

10

Met Glu Leu Arg Ala Ala

1

5

ctg gtc ctg gtg gtc ctc ctc atc gcc ggg ggt ctc ttc atg ttc acc 224
 Leu Val Leu Val Val Leu Leu Ile Ala Gly Gly Leu Phe Met Phe Thr

10

15

20

15

tac aag tcc aca cag ttc aac gtg gag ggc ttc gcc ttg gtg ctg ggg 272
 Tyr Lys Ser Thr Gln Phe Asn Val Glu Gly Phe Ala Leu Val Leu Gly

25

30

35

gcc tcg ttc atc ggt ggc att cgc tgg acc ctc acc cag atg ctc ctg 320
 Ala Ser Phe Ile Gly Gly Ile Arg Trp Thr Leu Thr Gln Met Leu Leu

20

40

45

50

cag aag gct gaa ctc ggc ctc cag aat ccc atc gac acc atg ttc cac 368
 Gln Lys Ala Glu Leu Gly Leu Gln Asn Pro Ile Asp Thr Met Phe His

55

60

65

70

ctg cag cca ctc atg ttc ctg ggg ctc ttc cct ctc ttt gct gta ttt 416

25

Leu Gln Pro Leu Met Phe Leu Gly Leu Phe Pro Leu Phe Ala Val Phe

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	75	80	85	
	gaa ggt ctc cat ttg tcc aca tct gag aaa atc ttc cgt ttc cag gac			464
	Glu Gly Leu His Leu Ser Thr Ser Glu Lys Ile Phe Arg Phe Gln Asp			
	90	95	100	
5	aca ggg ctg ctc ctg cgg gta ctt ggg agc ctc ttc ctt ggc ggg att			512
	Thr Gly Leu Leu Leu Arg Val Leu Gly Ser Leu Phe Leu Gly Gly Ile			
	105	110	115	
	ctc gcc ttt ggt ttg ggc ttc tct gag ttc ctc ctg gtc tcc aga acc			560
	Leu Ala Phe Gly Leu Gly Phe Ser Glu Phe Leu Leu Val Ser Arg Thr			
10	120	125	130	
	tcc agc ctc act ctc tcc att gcc ggc att ttt aag gaa gtc tgc act			608
	Ser Ser Leu Thr Leu Ser Ile Ala Gly Ile Phe Lys Glu Val Cys Thr			
	135	140	145	150
	ttg ctg ttg gca gct cat ctg ctg ggc gat cag atc agc ctc ctg aac			656
15	Leu Leu Leu Ala Ala His Leu Leu Gly Asp Gln Ile Ser Leu Leu Asn			
	155	160	165	
	tgg ctg ggc ttc gcc ctc tgc ctc tcg gga ata tcc ctc cac gtt gcc			704
	Trp Leu Gly Phe Ala Leu Cys Leu Ser Gly Ile Ser Leu His Val Ala			
	170	175	180	
20	ctc aaa gcc ctg cat tcc aga ggt aac cca gag tcc ctt cca gaa gcc			752
	Leu Lys Ala Leu His Ser Arg Gly Asn Pro Glu Ser Leu Pro Glu Ala			
	185	190	195	
	tct gtt ttc tgt tct tct ccc tgt gac tct tagtgattct gatgcaggaa			802
	Ser Val Phe Cys Ser Ser Pro Cys Asp Ser			
25	200	205		

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gtgtgcccgg tggctctgct gccgtcactc ctctaggaag atgtgggggt catctccaga 862
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cgccagggct catcatggta gctgggagct gtggacggga' gtcaccaggt ggtggggcca 1222
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15 gtcttaagcc aggcctcctt catcttctcg ctctgttag aacaccagtc ccctccccag 1702
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<210> 53

<211> 1402

20 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (60)..(1280)

25 <400> 53

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	atg gcg gca ggc gcc ggg gcc ggg tcc gcg ccg cgc tgg ctg agg gcg	107
	Met Ala Ala Gly Ala Gly Ala Gly Ser Ala Pro Arg Trp Leu Arg Ala	
	1 5 10 15	
5	ctg agc gag ccg ctg agc gcg gcg cag ctg cgg cga ctg gag gag cac	155
	Leu Ser Glu Pro Leu Ser Ala Ala Gln Leu Arg Arg Leu Glu Glu His	
	20 25 30	
	cgc tac agc gcg gcg ggc gtc tcg ctg ctc gag ccg ccg ctg cag ctc	203
	Arg Tyr Ser Ala Ala Gly Val Ser Leu Leu Glu Pro Pro Leu Gln Leu	
10	35 40 45	
	tac tgg acc tgg ctg ctc cag tgg atc ccg ctc tgg atg gcc ccc aac	251
	Tyr Trp Thr Trp Leu Leu Gln Trp Ile Pro Leu Trp Met Ala Pro Asn	
	50 55 60	
	tcc atc acc ctg ctg ggg ctc gcc gtc aac gtg gtc acc acg ctc gtg	299
15	Ser Ile Thr Leu Leu Gly Leu Ala Val Asn Val Val Thr Thr Leu Val	
	65 70 75 80	
	ctc atc tcc tac tgt ccc acg gcc acc gaa gag gca cca tac tgg aca	347
	Leu Ile Ser Tyr Cys Pro Thr Ala Thr Glu Glu Ala Pro Tyr Trp Thr	
	85 90 95	
20	tac ctt tta tgt gca ctg gga ctt ttt att tac cag tca ctg gat gct	395
	Tyr Leu Leu Cys Ala Leu Gly Leu Phe Ile Tyr Gln Ser Leu Asp Ala	
	100 105 110	
	att gat ggg aaa caa gcc aga aga aca aac tct tgt tcc cct tta ggg	443
	Ile Asp Gly Lys Gln Ala Arg Arg Thr Asn Ser Cys Ser Pro Leu Gly	
25	115 120 125	

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gag ctc ttt gac cat ggc tgt gac tct ctt tcc aca gta ttt atg gca 491
 Glu Leu Phe Asp His Gly Cys Asp Ser Leu Ser Thr Val Phe Met Ala
 130 135 140
 gtg gga gct tca att gcc gct cgc tta gga act tat cct gac tgg ttt 539
 5 Val Gly Ala Ser Ile Ala Ala Arg Leu Gly Thr Tyr Pro Asp Trp Phe
 145 150 155 160
 ttt ttc tgc tct ttt att ggg atg ttt gtg ttt tat tgc gct cat tgg 587
 Phe Phe Cys Ser Phe Ile Gly Met Phe Val Phe Tyr Cys Ala His Trp
 165 170 175
 10 cag act tat gtt tca ggc atg ttg aga ttt gga aaa gtg gat gta act 635
 Gln Thr Tyr Val Ser Gly Met Leu Arg Phe Gly Lys Val Asp Val Thr
 180 185 190
 gaa att cag ata gct tta gtg att gtc ttt gtg ttg tct gca ttt gga 683
 Glu Ile Gln Ile Ala Leu Val Ile Val Phe Val Leu Ser Ala Phe Gly
 15 195 200 205
 gga gca aca atg tgg gac tat acg att cct att cta gaa ata aaa ttg 731
 Gly Ala Thr Met Trp Asp Tyr Thr Ile Pro Ile Leu Glu Ile Lys Leu
 210 215 220
 aag atc ctt cca gtt ctt gga ttt cta ggt gga gta ata ttt tcc tgt 779
 20 Lys Ile Leu Pro Val Leu Gly Phe Leu Gly Gly Val Ile Phe Ser Cys
 225 230 235 240
 tca aat tat ttc cat gtt atc ctc cat ggt ggt gtt ggc aag aat gga 827
 Ser Asn Tyr Phe His Val Ile Leu His Gly Gly Val Gly Lys Asn Gly
 245 250 255
 25 tcc act ata gca ggc acc agt gtc ttg tca cct gga ctc cac ata gga 875

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Ser Thr Ile Ala Gly Thr Ser Val Leu Ser Pro Gly Leu His Ile Gly
 260 265 270
 cta att att ata ctg gca ata atg atc tat aaa aag tca gca act gat 923
 Leu Ile Ile Ile Leu Ala Ile Met Ile Tyr Lys Lys Ser Ala Thr Asp
 5 275 280 285
 gtg ttt gaa aag cat cct tgt ctt tat atc cta atg ttt gga tgt gtc 971
 Val Phe Glu Lys His Pro Cys Leu Tyr Ile Leu Met Phe Gly Cys Val
 290 295 300
 ttt gct aaa gtc tca caa aaa tta gtg gta gct cac atg acc aaa agt 1019
 10 Phe Ala Lys Val Ser Gln Lys Leu Val Val Ala His Met Thr Lys Ser
 305 310 315 320
 gaa cta tat ctt caa gac act gtc ttt ttg ggg cca ggt ctt ttg ttt 1067
 Glu Leu Tyr Leu Gln Asp Thr Val Phe Leu Gly Pro Gly Leu Leu Phe
 325 330 335
 15 tta gac cag tac ttt aat aac ttt ata gac gaa tat gtt gtt cta tgg 1115
 Leu Asp Gln Tyr Phe Asn Asn Phe Ile Asp Glu Tyr Val Val Leu Trp
 340 345 350
 atg gca atg gtg att tct tca ttt gat atg gtg ata tac ttt agt gct 1163
 Met Ala Met Val Ile Ser Ser Phe Asp Met Val Ile Tyr Phe Ser Ala
 20 355 360 365
 ttg tgc ctg caa att tca aga cac ctt cat cta aat ata ttc aag act 1211
 Leu Cys Leu Gln Ile Ser Arg His Leu His Leu Asn Ile Phe Lys Thr
 370 375 380
 gca tgt cat caa gca cct gaa cag gtt caa gtt ctt tct tca aag agt 1259
 25 Ala Cys His Gln Ala Pro Glu Gln Val Gln Val Leu Ser Ser Lys Ser

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385 390 395 400

cat cag aat aac atg gat tgaagagact tccgaacact tgctatctct 1307

His Gln Asn Asn Met Asp

405

5 tgctgctgct gtttcatgga aggagatatt aaacatttgt ttaattttta tttaagtgtt 1367

atacctatatt cagcaaataa aatatttcat tgctt 1402

<210> 54

<211> 2474

10 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (345)..(2201)

15 <400> 54

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tttaggagag gagcagacag ctcttagcta gggtcagatt tcaaattctc atctcttggt 120

gccaatacca ccaccagatt cttctttgaa gtcaactttt gagatcttca ctaagtacac 180

gttggtgtct gaagattcac acgagtgccct ctggtaatca ttttcttcag ggaatcacag 240

20 tctctcctct cagcaaagca tccactgtac tgaactttgc ttttggaaac atcttcttcc 300

tgagacctcg ttgaaagaaa ctctctggtg tcatactttc caat atg gag gtg aag 356

Met Glu Val Lys

1

aac ttt gca gtt tgg gat tat gtt gta ttt gca gcc ctc ttt ttc att 404

25 Asn Phe Ala Val Trp Asp Tyr Val Val Phe Ala Ala Leu Phe Phe Ile

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	5	10	15	20	
	tcc tct gga att ggg gtg ttc ttt gcc att aag gag aga aaa aag gca	452			
	Ser Ser Gly Ile Gly Val Phe Phe Ala Ile Lys Glu Arg Lys Lys Ala				
	25	30	35		
5	act tcc cga gag ttc ctg gtt ggg gga agg caa atg agc ttt ggc cct	500			
	Thr Ser Arg Glu Phe Leu Val Gly Gly Arg Gln Met Ser Phe Gly Pro				
	40	45	50		
	gtc ggc ttg tct ctg aca gcc agc ttc atg tca gct gtc acg gtc ctg	548			
	Val Gly Leu Ser Leu Thr Ala Ser Phe Met Ser Ala Val Thr Val Leu				
10	55	60	65		
	ggg acc cct tct gaa gtc tac cgc ttt ggg gca tcc ttc cta gtc ttc	596			
	Gly Thr Pro Ser Glu Val Tyr Arg Phe Gly Ala Ser Phe Leu Val Phe				
	70	75	80		
	ttc att gct tac cta ttt gtc atc ctc tta aca tca gag ctc ttt ctc	644			
15	Phe Ile Ala Tyr Leu Phe Val Ile Leu Leu Thr Ser Glu Leu Phe Leu				
	85	90	95	100	
	cct gtg ttc tac aga tct ggt atc acc agc act tat gag tac tta caa	692			
	Pro Val Phe Tyr Arg Ser Gly Ile Thr Ser Thr Tyr Glu Tyr Leu Gln				
	105	110	115		
20	cta cga ttc aac aaa cca gtt cgc tat gct gcc aca gtc atc tac att	740			
	Leu Arg Phe Asn Lys Pro Val Arg Tyr Ala Ala Thr Val Ile Tyr Ile				
	120	125	130		
	gta cag acg att ctc tac aca gga gtg gtg gtg tat gct cct gcc ctg	788			
	Val Gln Thr Ile Leu Tyr Thr Gly Val Val Val Tyr Ala Pro Ala Leu				
25	135	140	145		

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gca ctc aat caa gtg act ggg ttt gat ctc tgg ggc tct gtg ttt gca 836
 Ala Leu Asn Gln Val Thr Gly Phe Asp Leu Trp Gly Ser Val Phe Ala
 150 155 160
 aca gga att gtt tgc aca ttc tac tgt acc ctg gga gga tta aaa gca 884
 5 Thr Gly Ile Val Cys Thr Phe Tyr Cys Thr Leu Gly Gly Leu Lys Ala
 165 170 175 180
 gtg gtg tgg aca gat gca ttt cag atg gtt gtc atg att gtg ggc ttc 932
 Val Val Trp Thr Asp Ala Phe Gln Met Val Val Met Ile Val Gly Phe
 185 190 195
 10 tta acg gtt ctc att caa gga tca act cat gct ggg gga ttc cac aat 980
 Leu Thr Val Leu Ile Gln Gly Ser Thr His Ala Gly Gly Phe His Asn
 200 205 210
 gta tta gag caa tca aca aat gga tct cga cta cat ata ttt gac ttt 1028
 Val Leu Glu Gln Ser Thr Asn Gly Ser Arg Leu His Ile Phe Asp Phe
 15 215 220 225
 gat gta gat cct ctc agg cga cac act ttt tgg act atc aca gtg gga 1076
 Asp Val Asp Pro Leu Arg Arg His Thr Phe Trp Thr Ile Thr Val Gly
 230 235 240
 gga act ttt act tgg ctc gga atc tat ggg gtc aat caa tca act att 1124
 20 Gly Thr Phe Thr Trp Leu Gly Ile Tyr Gly Val Asn Gln Ser Thr Ile
 245 250 255 260
 cag cga tgc atc tct tgc aaa aca gaa aag cat gct aag ctt gcc ttg 1172
 Gln Arg Cys Ile Ser Cys Lys Thr Glu Lys His Ala Lys Leu Ala Leu
 265 270 275
 25 tat ttt aac ttg ctg ggt ctc tgg atc att ctg gtg tgt gct gtc ttc 1220

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Tyr Phe Asn Leu Leu Gly Leu Trp Ile Ile Leu Val Cys Ala Val Phe
 280 285 290
 tct ggc tta atc atg tac tct cac ttt aaa gac tgt gac cct tgg act 1268
 Ser Gly Leu Ile Met Tyr Ser His Phe Lys Asp Cys Asp Pro Trp Thr
 5 295 300 305
 tct ggc atc atc tca gca cca gac cag ctg atg ccg tac ttt gtc atg 1316
 Ser Gly Ile Ile Ser Ala Pro Asp Gln Leu Met Pro Tyr Phe Val Met
 310 315 320
 gag ata ttt gcc aca atg cca gga ctg cca gga ctt ttt gtg gct tgt 1364
 10 Glu Ile Phe Ala Thr Met Pro Gly Leu Pro Gly Leu Phe Val Ala Cys
 325 330 335 340
 gcc ttc agt gga act ctg agc acc gtg gct tcc agc atc aat gcc ttg 1412
 Ala Phe Ser Gly Thr Leu Ser Thr Val Ala Ser Ser Ile Asn Ala Leu
 345 350 355
 15 gca aca gtg acc ttt gag gat ttt gtc aag agc tgt ttt cct cat ctc 1460
 Ala Thr Val Thr Phe Glu Asp Phe Val Lys Ser Cys Phe Pro His Leu
 360 365 370
 tcc gac aag ctg agc acc tgg atc agt aaa ggc tta tgt ctc tta ttt 1508
 Ser Asp Lys Leu Ser Thr Trp Ile Ser Lys Gly Leu Cys Leu Leu Phe
 20 375 380 385
 ggc gtg atg tgt acc tct atg gct gtg gct gca tct gtc atg gga ggt 1556
 Gly Val Met Cys Thr Ser Met Ala Val Ala Ala Ser Val Met Gly Gly
 390 395 400
 gtt gtg cag gct tcc ctc agc att cac ggc atg tgt gga gga cca atg 1604
 25 Val Val Gln Ala Ser Leu Ser Ile His Gly Met Cys Gly Gly Pro Met

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	405	410	415	420	
	ctg ggc tta ttc tcc	ctg gga atc gtg ttc	cct ttt gtg aac tgg	aag	1652
	Leu Gly Leu Phe Ser	Leu Gly Ile Val Phe	Pro Phe Val Asn	Trp Lys	
	425	430	435		
5	ggt gca cta gga ggt	ctt ctt act gga atc	acc ttg tca ttt tgg	gtg	1700
	Gly Ala Leu Gly Gly	Leu Leu Thr Gly Ile	Thr Leu Ser Phe	Trp Val	
	440	445	450		
	gcc att ggg gcc ttc	att tac cct gca cca	gcc tct aag aca tgg	cct	1748
	Ala Ile Gly Ala Phe	Ile Tyr Pro Ala Pro	Ala Ser Lys Thr	Trp Pro	
10	455	460	465		
	ttg cct cta tca aca	gac caa tgt atc aaa	tca aat gtg aca gca	aca	1796
	Leu Pro Leu Ser Thr	Asp Gln Cys Ile Lys	Ser Asn Val Thr	Ala Thr	
	470	475	480		
	ggg cct cca gta cta	tcc agc aga cct gga	ata gct gat acc tgg	tac	1844
15	Gly Pro Pro Val Leu	Ser Ser Arg Pro Gly	Ile Ala Asp Thr	Trp Tyr	
	485	490	495	500	
	tcg atc tcc tac ctt	tac tac agt gca gtg	ggc tgc tta gga tgc	att	1892
	Ser Ile Ser Tyr Leu	Tyr Tyr Ser Ala Val	Gly Cys Leu Gly	Cys Ile	
	505	510	515		
20	gtt gct gga gta atc	atc agc ctc ata aca	ggc cgc caa aga ggt	gag	1940
	Val Ala Gly Val Ile	Ile Ser Leu Ile Thr	Gly Arg Gln Arg	Gly Glu	
	520	525	530		
	gat att caa cca ctg	tta att aga cca gtt	tgt aat tta ttt tgc	ttt	1988
	Asp Ile Gln Pro Leu	Leu Ile Arg Pro Val	Cys Asn Leu Phe	Cys Phe	
25	535	540	545		

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tgg tct aag aag tac aaa aca cta tgc tgg tgc gga gtt cag cat gac 2036
Trp Ser Lys Lys Tyr Lys Thr Leu Cys Trp Cys Gly Val Gln His Asp
550 555 560
agt ggg aca gag cag gaa aac ctt gag aat ggc agt gcc cgg aaa cag 2084
5 Ser Gly Thr Glu Gln Glu Asn Leu Glu Asn Gly Ser Ala Arg Lys Gln
565 570 575 580
ggg gct gaa tct gtc tta cag aac gga ctc aga aga gaa agc ctg gta 2132
Gly Ala Glu Ser Val Leu Gln Asn Gly Leu Arg Arg Glu Ser Leu Val
585 590 595
10 cat gtt cca ggc tat gat cct aag gac aaa agc tac aac aat atg gca 2180
His Val Pro Gly Tyr Asp Pro Lys Asp Lys Ser Tyr Asn Asn Met Ala
600 605 610
ttt gag act acc cat ttc taaggcaata cctgtatgaa tgcacacaca 2228
Phe Glu Thr Thr His Phe
15 615
cacgtgcaat acacacacac acacacaaac tccacatact tcttgcctac ttgttagtag 2288
atatgtatag ttgccattgc tagaagacag ggatgtctgg tgcctatttc tacttattta 2348
taactacatg caaaatgact gtctctcggg atattctttg aaagactcca actttcacag 2408
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20 gatttc 2474

<210> 55

<211> 3296

<212> DNA

25 <213> Homo sapiens

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<222> (142) .. (768)

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ccggctgcgc agaggagccg ctctcgccgc cgccacctcg gctgggagcc cacgaggctg 120
ccgcattctg cctctggaac a atg gga ctc ggc gcg cga ggt gct tgg gcc 171

1 5 10

15 20 25

15 30 35 40

45 50 55

20 Pro Ser Asp His Thr Asn Glu Thr Ser Asn Ser Thr Val Lys Pro Pro

75 80 85 90

25 cct aca gcg gca tct aat aca aca aca cca qgg atg qtc tca aca aat 459

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Pro Thr Ala Ala Ser Asn Thr Thr Thr Pro Gly Met Val Ser Thr Asn
 95 100 105
 atg act tct acc acc tta aag tct aca ccc aaa aca aca agt gtt tca 507
 Met Thr Ser Thr Thr Leu Lys Ser Thr Pro Lys Thr Thr Ser Val Ser
 5 110 115 120
 cag aac aca tct cag ata tca aca tcc aca atg acc gta acc cac aat 555
 Gln Asn Thr Ser Gln Ile Ser Thr Ser Thr Met Thr Val Thr His Asn
 125 130 135
 agt tca gtg aca tct gct gct tca tca gta aca atc aca aca act atg 603
 10 Ser Ser Val Thr Ser Ala Ala Ser Ser Val Thr Ile Thr Thr Thr Met
 140 145 150
 cat tct gaa gca aag aaa gga tca aaa ttt gat act ggg agc ttt gtt 651
 His Ser Glu Ala Lys Lys Gly Ser Lys Phe Asp Thr Gly Ser Phe Val
 155 160 165 170
 15 ggt ggt att gta tta acg ctg gga gtt tta tct att ctt tac att gga 699
 Gly Gly Ile Val Leu Thr Leu Gly Val Leu Ser Ile Leu Tyr Ile Gly
 175 180 185
 tgc aaa atg tat tac tca aga aga ggc att cgg tat cga acc ata gat 747
 Cys Lys Met Tyr Tyr Ser Arg Arg Gly Ile Arg Tyr Arg Thr Ile Asp
 20 190 195 200
 gaa cat gat gcc atc att taaggaaatc catggaccaa ggatggaata 795
 Glu His Asp Ala Ile Ile
 205
 cagattgatg ctgccctatc aattaatttt ggtttattaa tagtttaaaa caatattctc 855
 25 tttttgaaaa tagtataaac aggccatgca tataatgtac agtgtattac gtaaatatgt 915

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aaagattctt caaggtaaca agggtttggg ttttgaaata aacatctgga tcttatagac 975
cgttcataca atggttttag caagttcata gtaagacaaa caagtcctat cttttttttt 1035
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5 tcttttgtag ctacataaa gaacttcagt gcttttcaga gctggatata tcttaattac 1215
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caacattttt tgtgctttaa actgtagtag ttggtctaga aacaaaatac tccaagaaaa 1335
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ggagcattaa ggagcacata tttttattaa cttcttttga gctttcaatg ttgatgtaat 1455
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ccttcctgat ttggatattc cctcaaatcc ctctcttac tccatgctga aggagaagta 2055
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25 tacagagaac gctagatatt aagaatfff aaatggatca tttctacttg ctgtgcattt 2415

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ttgaagtagt ttagttatgt ctttttctct gtatgtaagt agtataatth gttactttca 2895
aatacccgta ctttgaatgt aggttttttt gttgttgta tctataaaaa ttgagggaaa 2955
10 tggttatgca aaaaaatatt ttgctttgga ccatatttct taagcataaa aaaaatgctc 3015
agttttgctt gcattccttg agaattgatt tatctgaaga tcaaaacaaa caatccagat 3075
gtataagtac taggcagaag ccaattttta aatttccttg aataatccat gaaaggaata 3135
attcaaatac agataaacag agttggcagt atattatagt gataattttg tattttcaca 3195
aaaaaaaaagt taaactcttc ttttcttttt attataatga ccagcttttg gtatttcatt 3255
15 gttaccaagt tctattttta gaataaaatt gttctccttc t 3296

<210> 56

<211> 1818

<212> DNA

20 <213> Homo sapiens

<220>

<221> CDS

<222> (26)..(1534)

<400> 56

25 aaaaaacccg cgcagtggcc cggcg atg tcg ctc gtg ctg cta agc ctg gcc 52

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	125	130	135	
	gcc cat aat att cct aat gca aat atg aat gaa gat ggc cct tcc atg			484
	Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly Pro Ser Met			
	140	145	150	
5	tct gtg aat ttc acc tca cca ggc tgc cta gac cac ata atg aaa tat			532
	Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile Met Lys Tyr			
	155	160	165	
	aaa aaa aag tgt gtc aag gcc gga agc ctg tgg gat ccg aac atc act			580
	Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr			
10	170	175	180	185
	gct tgt aag aag aat gag gag aca gta gaa gtg aac ttc aca acc act			628
	Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe Thr Thr Thr			
	190	195	200	
	ccc ctg gga aac aga tac atg gct ctt atc caa cac agc act atc atc			676
15	Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser Thr Ile Ile			
	205	210	215	
	ggg ttt tct cag gtg ttt gag cca cac cag aag aaa caa acg cga gct			724
	Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln Thr Arg Ala			
	220	225	230	
20	tca gtg gtg att cca gtg act ggg gat agt gaa ggt gct acg gtg cag			772
	Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala Thr Val Gln			
	235	240	245	
	ctg act cca tat ttt cct act tgt ggc agc gac tgc atc cga cat aaa			820
	Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile Arg His Lys			
25	250	255	260	265

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	gga aca gtt gtg ctc tgc cca caa aca ggc gtc cct ttc cct ctg gat	868
	Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe Pro Leu Asp	
	270 275 280	
	aac aac aaa agc aag ccg gga ggc tgg ctg cct ctc ctc ctg ctg tct	916
5	Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu Leu Leu Ser	
	285 290 295	
	ctg ctg gtg gcc aca tgg gtg ctg gtg gca ggg atc tat cta atg tgg	964
	Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile Tyr Leu Met Trp	
	300 305 310	
10	agg cac gaa agg atc aag aag act tcc ttt tct acc acc aca cta ctg	1012
	Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu	
	315 320 325	
	ccc ccc att aag gtt ctt gtg gtt tac cca tct gaa ata tgt ttc cat	1060
	Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile Cys Phe His	
15	330 335 340 345	
	cac aca att tgt tac ttc act gaa ttt ctt caa aac cat tgc aga agt	1108
	His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His Cys Arg Ser	
	350 355 360	
	gag gtc atc ctt gaa aag tgg cag aaa aag aaa ata gca gag atg ggt	1156
20	Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala Glu Met Gly	
	365 370 375	
	cca gtg cag tgg ctt gcc act caa aag aag gca gca gac aaa gtc gtc	1204
	Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp Lys Val Val	
	380 385 390	
25	ttc ctt ctt tcc aat gac gtc aac agt gtg tgc gat ggt acc tgt ggc	1252

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Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp Gly Thr Cys Gly
 395 400 405
 aag agc gag ggc agt ccc agt gag aac tct caa gac ctc ttc ccc ctt 1300
 Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu
 5 410 415 420 425
 gcc ttt aac ctt ttc tgc agt gat cta aga agc cag att cat ctg cac 1348
 Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile His Leu His
 430 435 440
 aaa tac gtg gtg gtc tac ttt aga gag att gat aca aaa gac gat tac 1396
 10 Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr
 445 450 455
 aat gct ctc agt gtc tgc ccc aag tac cac ctc atg aag gat gcc act 1444
 Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys Asp Ala Thr
 460 465 470
 15 gct ttc tgt gca gaa ctt ctc cat gtc aag cag cag gtg tca gca gga 1492
 Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val Ser Ala Gly
 475 480 485
 aaa aga tca caa gcc tgc cac gat ggc tgc tgc tcc ttg tagccccccc 1541
 Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu
 20 490 495 500
 atgagaagca agagacctta aaggcttcct atcccaccaa ttacaggga aaaacgtgtg 1601
 atgatacctga agcttactat gcagcctaca aacagcctta gtaattaaaa cattttatac 1661
 caataaaatt ttcaaatatt gctaactaat gtagcattaa ctaacgattg gaaactacat 1721
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 25 accattttga taatgcaaca ataaagcatc ttcagcc 1818

128/346

<210> 57

<211> 1646

<212> DNA

5 <213> Homo sapiens

<220>

<221> CDS

<222> (37)..(1047)

<400> 57

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                                     Met Arg Ala Pro Ser Met
                                     1           5
gac cgc gcg gcc gtg gcg agg gtg ggc gcg gta gcg agc gcc agc gtg   102
Asp Arg Ala Ala Val Ala Arg Val Gly Ala Val Ala Ser Ala Ser Val
15          10          15          20
tgc gcc ctg gtg gcg ggg gtg gtg ctg gct cag tac ata ttc acc ttg   150
Cys Ala Leu Val Ala Gly Val Val Leu Ala Gln Tyr Ile Phe Thr Leu
          25          30          35
aag agg aag acg ggg cgg aag acc aag atc atc gag atg atg cca gaa   198
20  Lys Arg Lys Thr Gly Arg Lys Thr Lys Ile Ile Glu Met Met Pro Glu
          40          45          50
ttc cag aaa agt tca gtt cga atc aag aac cct aca aga gta gaa gaa   246
Phe Gln Lys Ser Ser Val Arg Ile Lys Asn Pro Thr Arg Val Glu Glu
          55          60          65          70
25  att atc tgt ggt ctt atc aaa gga gga gct gcc aaa ctt cag ata ata   294

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Ile Ile Cys Gly Leu Ile Lys Gly Gly Ala Ala Lys Leu Gln Ile Ile
 75 80 85
 acg gac ttt gat atg aca ctc agt aga ttt tca tat aaa ggg aaa aga 342
 Thr Asp Phe Asp Met Thr Leu Ser Arg Phe Ser Tyr Lys Gly Lys Arg
 5 90 95 100
 tgc cca aca tgt cat aat atc att gac aac tgt aag ctg gtt aca gat 390
 Cys Pro Thr Cys His Asn Ile Ile Asp Asn Cys Lys Leu Val Thr Asp
 105 110 115
 gaa tgt aga aaa aag tta ttg caa cta aag gaa aaa tat tac gct att 438
 10 Glu Cys Arg Lys Lys Leu Leu Gln Leu Lys Glu Lys Tyr Tyr Ala Ile
 120 125 130
 gaa gtt gat cct gtt ctt act gta gaa gag aag tac cct tat atg gtg 486
 Glu Val Asp Pro Val Leu Thr Val Glu Glu Lys Tyr Pro Tyr Met Val
 135 140 145 150
 15 gaa tgg tat act aaa tca cat ggt ttg ctt gtt cag caa gct tta cca 534
 Glu Trp Tyr Thr Lys Ser His Gly Leu Leu Val Gln Gln Ala Leu Pro
 155 160 165
 aaa gct aaa ctt aaa gaa att gtg gca gaa tct gac gtt atg ctc aaa 582
 Lys Ala Lys Leu Lys Glu Ile Val Ala Glu Ser Asp Val Met Leu Lys
 20 170 175 180
 gaa gga tat gag aat ttc ttt gat aag ctc caa caa cat agc atc ccc 630
 Glu Gly Tyr Glu Asn Phe Phe Asp Lys Leu Gln Gln His Ser Ile Pro
 185 190 195
 gtg ttc ata ttt tcg gct gga atc ggc gat gta cta gag gaa gtt att 678
 25 Val Phe Ile Phe Ser Ala Gly Ile Gly Asp Val Leu Glu Glu Val Ile

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	200	205	210	
	cgt caa gct ggt gtt tat cat ccc aat gtc aaa gtt gtg tcc aat ttt	726		
	Arg Gln Ala Gly Val Tyr His Pro Asn Val Lys Val Val Ser Asn Phe			
	215	220	225	230
5	atg gat ttt gat gaa act ggg gtg ctc aaa gga ttt aaa gga gaa cta	774		
	Met Asp Phe Asp Glu Thr Gly Val Leu Lys Gly Phe Lys Gly Glu Leu			
	235	240	245	
	att cat gta ttt aac aaa cat gat ggt gcc ttg agg aat aca gaa tat	822		
	Ile His Val Phe Asn Lys His Asp Gly Ala Leu Arg Asn Thr Glu Tyr			
10	250	255	260	
	ttc aat caa cta aaa gac aat agt aac ata att ctt ctg gga gac tcc	870		
	Phe Asn Gln Leu Lys Asp Asn Ser Asn Ile Ile Leu Leu Gly Asp Ser			
	265	270	275	
	caa gga gac tta aga atg gca gat gga gtg gcc aat gtt gag cac att	918		
15	Gln Gly Asp Leu Arg Met Ala Asp Gly Val Ala Asn Val Glu His Ile			
	280	285	290	
	ctg aaa att gga tat cta aat gat aga gtg gat gag ctt tta gaa aag	966		
	Leu Lys Ile Gly Tyr Leu Asn Asp Arg Val Asp Glu Leu Leu Glu Lys			
	295	300	305	310
20	tac atg gac tct tat gat att gtt tta gta caa gat gaa tca tta gaa	1014		
	Tyr Met Asp Ser Tyr Asp Ile Val Leu Val Gln Asp Glu Ser Leu Glu			
	315	320	325	
	gta gcc aac tct att tta cag aag att cta taaacaagca ttctccaaga	1064		
	Val Ala Asn Ser Ile Leu Gln Lys Ile Leu			
25	330	335		

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agacctctct cctgtgggtg caattgaact gttcatccgt tcatcttgct gagagactta 1124
tttataatat atccttactc tcgaagtgtt ccctttgtat aactgaagta ttttcagata 1184
tggtgaatgc attgactgga agctcctttt ctccacctct ctcaacacac tcctcaccgt 1244
atcttttaac ccatttaaaa aaaaaaaaaa gctaaaatta gaaaaataac tccctacttt 1304
5 tccaaagtga attttgtagt ttaatgttat catgcagctt ttgaggagtc ttttactg 1364
ggaaagtttg tagaaatttt aaaataagtt ttatgaaatg gtgaaataat atgcatgatt 1424
ttaagtattg ccatttttgt aatttgggtt attatgctga tggatcacc atctcttgaa 1484
attgtgtagt gtttggttat tttgtctggg gaaaaaatat ttactggaaa agactagcag 1544
ttagtgttgg aaaaacctgg tgggtgttac aatgttgcta atcattacaa aacattctat 1604
10 attgaagcac tgataataaa tatgaaatgc aaaacctttt tt 1646

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<211> 1416

<212> DNA

15 <213> Homo sapiens

<220>

<221> CDS

<222> (174)..(1196)

<400> 58

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gcttgcccc caccgcggcc caggcaagcc accctgcccc cggccccac ctgcccgccc 120
cgctgcct tcctacccc ggtgcctgcg ggattgctgg agagaacgcg gcg atg 176

Met

1

25 gag ccg ggc agg acc cag ata aag ctt gac ccc agg tac aca gca gat 224

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Glu Pro Gly Arg Thr Gln Ile Lys Leu Asp Pro Arg Tyr Thr Ala Asp
 5 10 15
 ctt ctg gag gtg ctg aag acc aat tac ggc atc ccc tcc gcc tgc ttc 272
 Leu Leu Glu Val Leu Lys Thr Asn Tyr Gly Ile Pro Ser Ala Cys Phe
 5 20 25 30
 tct cag cct ccc aca gca gcc caa ctc ctg aga gcc ctg ggc cct gtg 320
 Ser Gln Pro Pro Thr Ala Ala Gln Leu Leu Arg Ala Leu Gly Pro Val
 35 40 45
 gaa ctt gcc ctc act agc atc ctg acc ttg ctg gcg ctg ggc tcc att 368
 10 Glu Leu Ala Leu Thr Ser Ile Leu Thr Leu Leu Ala Leu Gly Ser Ile
 50 55 60 65
 gcc atc ttc ctg gag gat gcc gtc tac ctg tac aag aac acc ctt tgc 416
 Ala Ile Phe Leu Glu Asp Ala Val Tyr Leu Tyr Lys Asn Thr Leu Cys
 70 75 80
 15 ccc atc aag agg cgg act ctg ctc tgg aag agc tcg gca ccc acg gtg 464
 Pro Ile Lys Arg Arg Thr Leu Leu Trp Lys Ser Ser Ala Pro Thr Val
 85 90 95
 gtg tct gtg ctg tgc tgc ttt ggt ctc tgg atc cct cgt tcc ctg gtg 512
 Val Ser Val Leu Cys Cys Phe Gly Leu Trp Ile Pro Arg Ser Leu Val
 20 100 105 110
 ctg gtg gaa atg acc atc acc tcg ttt tat gcc gtg tgc ttt tac ctg 560
 Leu Val Glu Met Thr Ile Thr Ser Phe Tyr Ala Val Cys Phe Tyr Leu
 115 120 125
 ctg atg ctg gtc atg gtg gaa ggc ttt ggg ggg aag gag gca gtg ctg 608
 25 Leu Met Leu Val Met Val Glu Gly Phe Gly Gly Lys Glu Ala Val Leu

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	130	135	140	145	
	agg acg ctg agg gac acc ccg atg atg gtc cac aca ggc ccc tgc tgc	656			
	Arg Thr Leu Arg Asp Thr Pro Met Met Val His Thr Gly Pro Cys Cys				
	150	155	160		
5	tgc tgc tgc ccc tgc tgt cca cgg ctg ctg ctc acc agg aag aag ctt	704			
	Cys Cys Cys Pro Cys Cys Pro Arg Leu Leu Leu Thr Arg Lys Lys Leu				
	165	170	175		
	cag ctg ctg atg ttg ggc cct ttc caa tac gcc ttc ttg aag ata acg	752			
	Gln Leu Leu Met Leu Gly Pro Phe Gln Tyr Ala Phe Leu Lys Ile Thr				
10	180	185	190		
	ctg acc ctg gtg ggc ctg ttt ctc atc ccc gac ggc atc tat gac cca	800			
	Leu Thr Leu Val Gly Leu Phe Leu Ile Pro Asp Gly Ile Tyr Asp Pro				
	195	200	205		
	gca gac att tct gag ggg agc aca gct cta tgg atc aac act ttc ctt	848			
15	Ala Asp Ile Ser Glu Gly Ser Thr Ala Leu Trp Ile Asn Thr Phe Leu				
	210	215	220	225	
	ggc gtg tcc aca ctg ctg gct ctc tgg acc ctg ggc atc att tcc cgt	896			
	Gly Val Ser Thr Leu Leu Ala Leu Trp Thr Leu Gly Ile Ile Ser Arg				
	230	235	240		
20	caa gcc agg cta cac ctg ggt gag cag aac atg gga gcc aaa ttt gct	944			
	Gln Ala Arg Leu His Leu Gly Glu Gln Asn Met Gly Ala Lys Phe Ala				
	245	250	255		
	ctg ttc cag gtt ctc ctc atc ctg act gcc cta cag ccc tcc atc ttc	992			
	Leu Phe Gln Val Leu Leu Ile Leu Thr Ala Leu Gln Pro Ser Ile Phe				
25	260	265	270		

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tca gtc ttg gcc aac ggt ggg cag att gct tgt tcg cct ccc tat tcc 1040
 Ser Val Leu Ala Asn Gly Gly Gln Ile Ala Cys Ser Pro Pro Tyr Ser
 275 280 285
 tct aaa acc agg tct caa gtg atg aat tgc cac ctc ctc ata ctg gag 1088
 5 Ser Lys Thr Arg Ser Gln Val Met Asn Cys His Leu Leu Ile Leu Glu
 290 295 300 305
 act ttt cta atg act gtg ctg aca cga atg tac tac cga agg aaa gac 1136
 Thr Phe Leu Met Thr Val Leu Thr Arg Met Tyr Tyr Arg Arg Lys Asp
 310 315 320
 10 cac aag gtt ggg tat gaa act ttc tct tct cca gac ctg gac ttg aac 1184
 His Lys Val Gly Tyr Glu Thr Phe Ser Ser Pro Asp Leu Asp Leu Asn
 325 330 335
 ctc aaa gcc taaggtggat ggcttggaca atgaaaggat gctgtactca 1233
 Leu Lys Ala
 15 340
 ttagaataca agattccttt actgtccctc aaccttgacc aaatgggaag cattccccct 1293
 tgtcaacaca agctggcaga tacatttgac tctacagatg aaggtgaaca atgttagaat 1353
 aaaattgctt tggatcttgc ctggaagggtg ttttaagttt tgtaataaac aagatgatgt 1413
 ctg 1416
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 <211> 1927
 <212> DNA
 <213> Homo sapiens
 25 <220>

135/346

<221> CDS

<222> (89)..(760)

<400> 59

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Met Leu Trp Arg Gln Leu Ile Tyr

1 5
tggtcaa ctg ctg gct ttg ttt ttc ctc cct ttt tgc ctg tgt caa gat 160
Trp Gln Leu Leu Ala Leu Phe Phe Leu Pro Phe Cys Leu Cys Gln Asp
10 10 15 20
gaa tac atg gag gtg agc gga aga act aat aaa gtg gtg gca aga ata 208
Glu Tyr Met Glu Val Ser Gly Arg Thr Asn Lys Val Val Ala Arg Ile
25 30 35 40
gtg caa agc cac cag cag act ggc cgt agc ggc tcc agg agg gag aaa 256
15 Val Gln Ser His Gln Gln Thr Gly Arg Ser Gly Ser Arg Arg Glu Lys
45 50 55
gtg aga gag cgg agc cat cct aaa act ggg act gtg gat aat aac act 304
Val Arg Glu Arg Ser His Pro Lys Thr Gly Thr Val Asp Asn Asn Thr
60 65 70
20 tct aca gac cta aaa tcc ctg aga cca gat gag cta ccg cac ccc gag 352
Ser Thr Asp Leu Lys Ser Leu Arg Pro Asp Glu Leu Pro His Pro Glu
75 80 85
gta gat gac cta gcc cag atc acc aca ttc tgg ggc cag tct cca caa 400
Val Asp Asp Leu Ala Gln Ile Thr Thr Phe Trp Gly Gln Ser Pro Gln
25 90 95 100

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acc gga gga cta ccc cca gac tgc agt aag tgt tgt cat gga gac tac 448
 Thr Gly Gly Leu Pro Pro Asp Cys Ser Lys Cys Cys His Gly Asp Tyr
 105 110 115 120
 agc ttt cga ggc tac caa ggc ccc cct ggg cca ccg ggc cct cct ggc 496
 Ser Phe Arg Gly Tyr Gln Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
 125 130 135
 att cca gga aac cat gga aac aat ggc aac aat gga gcc act ggt cat 544
 Ile Pro Gly Asn His Gly Asn Asn Gly Asn Asn Gly Ala Thr Gly His
 140 145 150
 10 gaa gga gcc aaa ggt gag aag ggc gac aaa ggt gac ctg ggg cct cga 592
 Glu Gly Ala Lys Gly Glu Lys Gly Asp Lys Gly Asp Leu Gly Pro Arg
 155 160 165
 ggg gag ggg ggg cag cat ggc ccc aaa gga gag aag ggc tac ccg ggg 640
 Gly Glu Arg Gly Gln His Gly Pro Lys Gly Glu Lys Gly Tyr Pro Gly
 15 170 175 180
 att cca cca gat ctt cag att gca ttc atg gct tct ctg gca acc cac 688
 Ile Pro Pro Glu Leu Gln Ile Ala Phe Met Ala Ser Leu Ala Thr His
 185 190 195 200
 ttc agc aat cag aac aat ggg att atc ttc agc agt gtt gag acc aac 736
 20 Phe Ser Asn Gln Asn Ser Gly Ile Ile Phe Ser Ser Val Glu Thr Asn
 205 210 215
 att gga aac ttc ttg atg tca gactggtag atttggggcc ccagtatcag 787
 Ile Gly Asn Phe Leu Met Ser
 220
 25 gtgtgtattt cttcaccttc agcatgatga agc tgagga tggtgaggaa gtgtatgtgt 847

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accttatgca caatggcaac acagtcttca gcatgtacag ctatgaaatg aaggggcaaat 907
cagatacatc cagcaatcat gctgtgctga agctagccaa aggggatgag gtttggtgc 967
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atatctgaag aacatacact attaataaat accttagaga aagattttga cctggcttta 1867
gataaaactg tggcaagaaa aatgtaatga gcaatatatg gaaataaaca cacctttggt 1927

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<211> 1419
<212> DNA
<213> Homo sapiens
<220>
25 <221> CDS

138/346

<222> (172)..(1101)

<400> 60

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5  gacccgctcc aaccctcggg tcttctgca atacagtga tacaatttgt c atg gct 177

Met Ala

1

act ctg agt gtt ata ggt tca agt tca ctt att gcc tat gct gta ttc 225
Thr Leu Ser Val Ile Gly Ser Ser Ser Leu Ile Ala Tyr Ala Val Phe
10      5      10      15
cat aat ata cag aaa tct cca gag ata aga cca ctt ttt tat ctg agc 273
His Asn Ile Gln Lys Ser Pro Glu Ile Arg Pro Leu Phe Tyr Leu Ser
20      25      30
ttc tgt gac ctg ctc ctg gga ctt tgc tgg ctc acg gag aca ctt ctc 321
15  Phe Cys Asp Leu Leu Leu Gly Leu Cys Trp Leu Thr Glu Thr Leu Leu
35      40      45      50
tat gga gct tca gta gca aat aag gac atc atc tgc tat aac cta caa 369
Tyr Gly Ala Ser Val Ala Asn Lys Asp Ile Ile Cys Tyr Asn Leu Gln
55      60      65
20  gca gtt gga cag ata ttc tac att tcc tca ttt ctc tac acc gtc aat 417
Ala Val Gly Gln Ile Phe Tyr Ile Ser Ser Phe Leu Tyr Thr Val Asn
70      75      80
tac atc tgg tat ttg tac aca gag ctg agg atg aaa cac acc cag agt 465
Tyr Ile Trp Tyr Leu Tyr Thr Glu Leu Arg Met Lys His Thr Gln Ser
25      85      90      95

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gga cag agc aca tct cca ctg gtg ata gat tat act tgt cga gtt tgt 513
 Gly Gln Ser Thr Ser Pro Leu Val Ile Asp Tyr Thr Cys Arg Val Cys
 100 105 110
 caa atg gcc ttt gtt ttc tca agg tgt atc ttg atg cac tca cca cca 561
 5 Gln Met Ala Phe Val Phe Ser Arg Cys Ile Leu Met His Ser Pro Pro
 115 120 125 130
 tca gcc atg gct gaa ctt cca cct tct gcc aac aca tct gtc tgt agc 609
 Ser Ala Met Ala Glu Leu Pro Pro Ser Ala Asn Thr Ser Val Cys Ser
 135 140 145
 10 aca ctt tat ttt tat ggt atc gcc att ttc ctg ggc agc ttt gta ctc 657
 Thr Leu Tyr Phe Tyr Gly Ile Ala Ile Phe Leu Gly Ser Phe Val Leu
 150 155 160
 agc ctc ctt acc att atg gtc tta ctt atc cga gcc cag aca ttg tat 705
 Ser Leu Leu Thr Ile Met Val Leu Leu Ile Arg Ala Gln Thr Leu Tyr
 165 170 175
 15 aag aag ttt gtg aag tca act ggc ttt ctg ggg agt gaa cag tgg gca 753
 Lys Lys Phe Val Lys Ser Thr Gly Phe Leu Gly Ser Glu Gln Trp Ala
 180 185 190
 gtg att cac att gtg gac caa cgg gtg cgc ttc tac cca gtg gcc ttc 801
 20 Val Ile His Ile Val Asp Gln Arg Val Arg Phe Tyr Pro Val Ala Phe
 195 200 205 210
 ttt tgc tgc tgg ggc cca gct gtc att cta atg atc ata aag ctg act 849
 Phe Cys Cys Trp Gly Pro Ala Val Ile Leu Met Ile Ile Lys Leu Thr
 215 220 225
 25 aag cca cag gac acc aag ctt cac atg gcc ctt tat gtt ctc cag gct 897

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Lys Pro Gln Asp Thr Lys Leu His Met Ala Leu Tyr Val Leu Gln Ala
 230 235 240
 cta acg gca aca tct cag ggt cta ctc aac tgt gga gta tat ggc tgg 945
 Leu Thr Ala Thr Ser Gln Gly Leu Leu Asn Cys Gly Val Tyr Gly Trp
 5 245 250 255
 acg cag cac aaa ttc cac caa cta aag cag gag gct cgg cgt gat gca 993
 Thr Gln His Lys Phe His Gln Leu Lys Gln Glu Ala Arg Arg Asp Ala
 260 265 270
 gat acc cag aca cca tta tta tgc tca cag aag aga ttc tat agc agg 1041
 10 Asp Thr Gln Thr Pro Leu Leu Cys Ser Gln Lys Arg Phe Tyr Ser Arg
 275 280 285 290
 ggc tta aat tca ctg gaa tcc acc ctg act ttt cct gcc agt act tct 1089
 Gly Leu Asn Ser Leu Glu Ser Thr Leu Thr Phe Pro Ala Ser Thr Ser
 295 300 305
 15 acc att ttt tgaaactaca atactggaac atccaggaac tggagttatt 1138
 Thr Ile Phe
 ctacgcta at ggattggaaa gaatgttggg aaaggacatc ttaaattctt tctaactatg 1198
 ccctaaactg cagaactcaa aggaaatata gtgccattgt tagtagtcat tctagatgaa 1258
 ttgggagtat ctctccagtt attcccagat tcactagtga tccttaaagt ctctattcag 1318
 20 ggagaggaag acactttcca tctcagagat agactcgtgt taccttgatg gatattggat 1378
 ttgtctaagt ctcttctaga aaaaataaat tctagattat t 1419

 <210> 61
 <211> 599
 25 <212> PRT

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<213> Homo sapiens

<400> 61

Met Pro Ser Ser Leu Pro Gly Ser Gln Val Pro His Pro Thr Leu Asp
 5 1 5 10 15
 Ala Val Asp Leu Val Glu Lys Thr Leu Arg Asn Glu Gly Thr Ser Ser
 20 25 30
 Ser Ala Pro Val Leu Glu Glu Gly Asp Thr Asp Pro Trp Thr Leu Pro
 35 40 45
 10 Gln Leu Lys Asp Thr Ser Gln Pro Trp Lys Glu Leu Arg Val Ala Gly
 50 55 60
 Arg Leu Arg Arg Val Ala Gly Ser Val Leu Lys Ala Cys Gly Leu Leu
 65 70 75 80
 Gly Ser Leu Tyr Phe Phe Ile Cys Ser Leu Asp Val Leu Ser Ser Ala
 15 85 90 95
 Phe Gln Leu Leu Gly Ser Lys Val Ala Gly Asp Ile Phe Lys Asp Asn
 100 105 110
 Val Val Leu Ser Asn Pro Val Ala Gly Leu Val Ile Gly Val Leu Val
 115 120 125
 20 Thr Ala Leu Val Gln Ser Ser Ser Thr Ser Ser Ser Ile Val Val Ser
 130 135 140
 Met Val Ala Ala Lys Leu Leu Thr Val Arg Val Ser Val Pro Ile Ile
 145 150 155 160
 Met Gly Val Asn Val Gly Thr Ser Ile Thr Ser Thr Leu Val Ser Met
 25 165 170 175

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	Ala	Gln	Ser	Gly	Asp	Arg	Asp	Glu	Phe	Gln	Arg	Ala	Phe	Ser	Gly	Ser	
																	180 185 190
	Ala	Val	His	Gly	Ile	Phe	Asn	Trp	Leu	Thr	Val	Leu	Val	Leu	Leu	Pro	
																	195 200 205
5	Leu	Glu	Ser	Ala	Thr	Ala	Leu	Leu	Glu	Arg	Leu	Ser	Glu	Leu	Ala	Leu	
																	210 215 220
	Gly	Ala	Ala	Ser	Leu	Thr	Pro	Arg	Ala	Gln	Ala	Pro	Asp	Ile	Leu	Lys	
																	225 230 235 240
	Val	Leu	Thr	Lys	Pro	Leu	Thr	His	Leu	Ile	Val	Gln	Leu	Asp	Ser	Asp	
10																	245 250 255
	Met	Ile	Met	Ser	Ser	Ala	Thr	Gly	Asn	Ala	Thr	Asn	Ser	Ser	Leu	Ile	
																	260 265 270
	Lys	His	Trp	Cys	Gly	Thr	Thr	Gly	Gln	Pro	Thr	Gln	Glu	Asn	Ser	Ser	
																	275 280 285
15	Cys	Gly	Ala	Phe	Gly	Pro	Cys	Thr	Glu	Lys	Asn	Ser	Thr	Ala	Pro	Ala	
																	290 295 300
	Asp	Arg	Leu	Pro	Cys	Arg	His	Leu	Phe	Ala	Gly	Thr	Glu	Leu	Thr	Asp	
																	305 310 315 320
	Leu	Ala	Val	Gly	Cys	Ile	Leu	Leu	Ala	Gly	Ser	Leu	Leu	Val	Leu	Cys	
20																	325 330 335
	Gly	Cys	Leu	Val	Leu	Ile	Val	Lys	Leu	Leu	Asn	Ser	Val	Leu	Arg	Gly	
																	340 345 350
	Arg	Val	Ala	Gln	Val	Val	Arg	Thr	Val	Ile	Asn	Ala	Asp	Phe	Pro	Phe	
																	355 360 365
25	Pro	Leu	Gly	Trp	Leu	Gly	Gly	Tyr	Leu	Ala	Val	Leu	Ala	Gly	Ala	Gly	

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	370	375	380	
	Leu Thr Phe Ala Leu Gln Ser Ser Ser Val Phe Thr Ala Ala Val Val			
	385	390	395	400
	Pro Leu Met Gly Val Gly Val Ile Ser Leu Asp Arg Ala Tyr Pro Leu			
5	405	410	415	
	Leu Leu Gly Ser Asn Ile Gly Thr Thr Thr Thr Ala Leu Leu Ala Ala			
	420	425	430	
	Leu Ala Ser Pro Ala Asp Arg Met Leu Ser Ala Leu Gln Val Ala Leu			
	435	440	445	
10	Ile His Phe Phe Phe Asn Leu Ala Gly Ile Leu Leu Trp Tyr Leu Val			
	450	455	460	
	Pro Ala Leu Arg Leu Pro Ile Pro Leu Ala Arg His Phe Gly Val Val			
	465	470	475	480
	Thr Ala Arg Tyr Arg Trp Val Ala Gly Val Tyr Leu Leu Leu Gly Phe			
15	485	490	495	
	Leu Leu Leu Pro Leu Ala Ala Phe Gly Leu Ser Leu Ala Gly Gly Met			
	500	505	510	
	Val Leu Ala Ala Val Gly Gly Pro Leu Val Gly Leu Val Leu Leu Val			
	515	520	525	
20	Ile Leu Val Thr Val Leu Gln Arg Arg Arg Pro Ala Trp Leu Pro Val			
	530	535	540	
	Arg Leu Arg Ser Trp Ala Trp Leu Pro Val Trp Leu His Ser Leu Glu			
	545	550	555	560
	Pro Trp Asp Arg Leu Val Thr Arg Cys Cys Pro Cys Asn Val Cys Ser			
25	565	570	575	

144/346

Pro Pro Lys Ala Thr Thr Lys Glu Ala Tyr Cys Tyr Glu Asn Pro Glu

580

585

590

Ile Leu Ala Ser Gln Gln Leu

595

5

<210> 62

<211> 81

<212> PRT

<213> Homo sapiens

10

<400> 62

Met Asp Gly Gly Gln Pro Ile Pro Ser Ser Leu Val Pro Leu Gly Asn

1

5

10

15

Glu Ser Ala Asp Ser Ser Met Ser Leu Glu Gln Lys Met Thr Phe Val

15

20

25

30

Phe Val Ile Leu Leu Phe Ile Phe Leu Gly Ile Leu Ile Val Arg Cys

35

40

45

Phe Arg Ile Leu Leu Asp Pro Tyr Arg Ser Met Pro Thr Ser Thr Trp

50

55

60

20

Ala Asp Gly Leu Glu Gly Leu Glu Lys Gly Gln Phe Asp His Ala Leu

65

70

75

80

Ala

25

<210> 63

145/346

<211> 654

<212> PRT

<213> Homo sapiens

5 <400> 63

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu

1 5 10 15

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val

20 25 30

10 Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr

35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala

50 55 60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe

15 65 70 75 80

Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe

85 90 95

Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala

100 105 110

20 Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp

115 120 125

Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His

130 135 140

Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe

25 145 150 155 160

146/346

	Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly		
	165	170	175
	Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala		
	180	185	190
5	Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu		
	195	200	205
	Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu		
	210	215	220
	Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro		
10	225	230	235
	Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro		
	245	250	255
	His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr		
	260	265	270
15	Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly		
	275	280	285
	Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe		
	290	295	300
	His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly		
20	305	310	315
	Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser		
	325	330	335
	Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile		
	340	345	350
25	Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro		

147/346

	355		360		365
	Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu				
	370		375		380
	Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu				
5	385		390		395
	Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr				400
		405		410	415
	Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val				
		420		425	430
10	Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val				
		435		440	445
	Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr				
		450		455	460
	Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg				
15	465		470		475
	Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro				480
		485		490	495
	Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu				
		500		505	510
20	Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys				
		515		520	525
	Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr				
		530		535	540
	Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly				
25	545		550		555
					560

148/346

Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr
565 570 575

Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu
580 585 590

5 Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu
595 600 605

Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu
610 615 620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala
10 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
645 650

<210> 64

15 <211> 390

<212> PRT

<213> Homo sapiens

<400> 64

20 Met Gly Met Asp Asp Cys Asp Ser Phe Phe Pro Gly Pro Leu Val Ala
1 5 10 15

Ile Ile Cys Asp Ile Leu Gly Glu Lys Thr Thr Ser Ile Leu Gly Ala
20 25 30

Phe Val Val Thr Gly Gly Tyr Leu Ile Ser Ser Trp Ala Thr Ser Ile
25 35 40 45

149/346

Pro Phe Leu Cys Val Thr Met Gly Leu Leu Pro Gly Leu Gly Ser Ala
 50 55 60
 Phe Leu Tyr Gln Val Ala Ala Val Val Thr Thr Lys Tyr Phe Lys Lys
 65 70 75 80
 5 Arg Leu Ala Leu Ser Thr Ala Ile Ala Arg Ser Gly Met Gly Leu Thr
 85 90 95
 Phe Leu Leu Ala Pro Phe Thr Lys Phe Leu Ile Asp Leu Tyr Asp Trp
 100 105 110
 Thr Gly Ala Leu Ile Leu Phe Gly Ala Ile Ala Leu Asn Leu Val Pro
 10 115 120 125
 Ser Ser Met Leu Leu Arg Pro Ile His Ile Lys Ser Glu Asn Asn Ser
 130 135 140
 Gly Ile Lys Asp Lys Gly Ser Ser Leu Ser Ala His Gly Pro Glu Ala
 145 150 155 160
 15 His Ala Thr Glu Thr His Cys His Glu Thr Glu Glu Ser Thr Ile Lys
 165 170 175
 Asp Ser Thr Thr Gln Lys Ala Gly Leu Pro Ser Lys Asn Leu Thr Val
 180 185 190
 Ser Gln Asn Gln Ser Glu Glu Phe Tyr Asn Gly Pro Asn Arg Asn Arg
 20 195 200 205
 Leu Leu Leu Lys Ser Asp Glu Glu Ser Asp Lys Val Ile Ser Trp Ser
 210 215 220
 Cys Lys Gln Leu Phe Asp Ile Ser Leu Phe Arg Asn Pro Phe Phe Tyr
 225 230 235 240
 25 Ile Phe Thr Trp Ser Phe Leu Leu Ser Gln Leu Ala Tyr Phe Ile Pro

150/346

245 250 255
Thr Phe His Leu Val Ala Arg Ala Lys Thr Leu Gly Ile Asp Ile Met
260 265 270
Asp Ala Ser Tyr Leu Val Ser Val Ala Gly Ile Leu Glu Thr Val Ser
5 275 280 285
Gln Ile Ile Ser Gly Trp Val Ala Asp Gln Asn Trp Ile Lys Lys Tyr
290 295 300
His Tyr His Lys Ser Tyr Leu Ile Leu Cys Gly Ile Thr Asn Leu Leu
305 310 315 320
10 Ala Pro Leu Ala Thr Thr Phe Pro Leu Leu Met Thr Tyr Thr Ile Cys
325 330 335
Phe Ala Ile Phe Ala Gly Gly Tyr Leu Ala Leu Ile Leu Pro Val Leu
340 345 350
Val Asp Leu Cys Arg Asn Ser Thr Val Asn Arg Phe Leu Gly Leu Ala
15 355 360 365
Ser Phe Phe Ala Gly Met Ala Val Leu Ser Gly Pro Pro Ile Ala Gly
370 375 380
Asn Thr Phe Thr Thr Phe
385 390
20
<210> 65
<211> 452
<212> PRT
<213> Homo sapiens
25

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<400> 65

	Met	Glu	Leu	Ala	Leu	Arg	Arg	Ser	Pro	Val	Pro	Arg	Trp	Leu	Leu	Leu
	1				5						10				15	
	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp	Trp	Pro
5					20					25					30	
	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val	Arg	Lys	Asp
				35				40					45			
	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn	Ser	Cys	Lys	Asn
		50					55						60			
10	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln	Gly	Gly	Pro	Gly	Gly
	65					70					75				80	
	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu	Ile	Gly	Pro	Leu	Asp	Ser
					85						90				95	
	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp	Leu	Gln	Ala	Ala	Ser	Leu	Leu
15				100						105					110	
	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser
				115						120					125	
	Gly	Ala	Tyr	Ala	Lys	Asp	Leu	Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val
		130						135						140		
20	Leu	Leu	Lys	Thr	Phe	Phe	Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro
	145					150					155				160	
	Phe	Tyr	Ile	Phe	Ser	Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile
					165						170				175	
	Gly	Leu	Glu	Leu	Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn
25				180						185					190	

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Phe Ala Gly Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser
 195 200 205
 Val Leu Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp
 210 215 220
 5 Lys Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala
 225 230 235 240
 Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys Ala
 245 250 255
 Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr Asn Ile
 10 260 265 270
 Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser Leu Glu Phe
 275 280 285
 Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His Val Arg His Leu
 290 295 300
 15 Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly Pro Ile Arg Lys Lys
 305 310 315 320
 Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp Gly Gly Gln Ala Thr Asn
 325 330 335
 Val Phe Val Asn Met Glu Glu Asp Phe Met Lys Pro Val Ile Ser Ile
 20 340 345 350
 Val Asp Glu Leu Leu Glu Ala Gly Ile Asn Val Thr Val Tyr Asn Gly
 355 360 365
 Gln Leu Asp Leu Ile Val Asp Thr Met Gly Gln Glu Ala Trp Val Arg
 370 375 380
 25 Lys Leu Lys Trp Pro Glu Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys

153/346

385 390 395 400
Ala Leu Tyr Ser Asp Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys
405 410 415
Ser Tyr Lys Asn Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met
5 420 425 430
Val Pro Ser Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val
435 440 445
Thr Gln Gln Glu
450
10
<210> 66
<211> 490
<212> PRT
<213> Homo sapiens
15
<400> 66
Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
1 5 10 15
Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
20 20 25 30
Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
35 40 45
Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
50 55 60
25 Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly

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	65		70		75		80									
	Pro	Gly	Pro	Gly	Gly	Gly	Ser	Lys	Asp	Leu	Leu	Phe	Trp	Val	Ala	Leu
				85					90							95
	Glu	Arg	Arg	Arg	Ser	His	Cys	Thr	Leu	Glu	Asn	Glu	Pro	Leu	Arg	Gly
5				100					105							110
	Phe	Ser	Trp	Leu	Ser	Ser	Asp	Pro	Gly	Gly	Leu	Glu	Ser	Asp	Thr	Leu
				115					120							125
	Gln	Trp	Val	Glu	Glu	Pro	Gln	Arg	Ser	Cys	Thr	Ala	Arg	Arg	Cys	Ala
				130					135							140
10	Val	Leu	Gln	Ala	Thr	Gly	Gly	Val	Glu	Pro	Ala	Gly	Trp	Lys	Glu	Met
				145					150							155
	Arg	Cys	His	Leu	Arg	Ala	Asn	Gly	Tyr	Leu	Cys	Lys	Tyr	Gln	Phe	Glu
							165						170			175
	Val	Leu	Cys	Pro	Ala	Pro	Arg	Pro	Gly	Ala	Ala	Ser	Asn	Leu	Ser	Tyr
15				180					185							190
	Arg	Ala	Pro	Phe	Gln	Leu	His	Ser	Ala	Ala	Leu	Asp	Phe	Ser	Pro	Pro
				195					200							205
	Gly	Thr	Glu	Val	Ser	Ala	Leu	Cys	Arg	Gly	Gln	Leu	Pro	Ile	Ser	Val
				210					215							220
20	Thr	Cys	Ile	Ala	Asp	Glu	Ile	Gly	Ala	Arg	Trp	Asp	Lys	Leu	Ser	Gly
				225					230							235
	Asp	Val	Leu	Cys	Pro	Cys	Pro	Gly	Arg	Tyr	Leu	Arg	Ala	Gly	Lys	Cys
							245						250			255
	Ala	Glu	Leu	Pro	Asn	Cys	Leu	Asp	Asp	Leu	Gly	Gly	Phe	Ala	Cys	Glu
25				260					265							270

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Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr
 275 280 285
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg
 290 295 300
 5 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro
 305 310 315 320
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln
 325 330 335
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln
 10 340 345 350
 Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala
 355 360 365
 Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr
 370 375 380
 15 Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe
 385 390 395 400
 Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr
 405 410 415
 Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln
 20 420 425 430
 Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu
 435 440 445
 Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val
 450 455 460
 25 Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu

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465 470 475 480
Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala
 485 490

5 <210> 67
 <211> 392
 <212> PRT
 <213> Homo sapiens

10 <400> 67
Met Gln Val Asn Thr Thr Lys Phe Met Leu Leu Tyr Ala Trp Tyr Ser
 1 5 10 15
Trp Pro Asn Val Val Leu Cys Phe Phe Gly Gly Phe Leu Ile Asp Arg
 20 25 30
15 Val Phe Gly Ile Arg Trp Gly Thr Ile Ile Phe Ser Cys Phe Val Cys
 35 40 45
Ile Gly Gln Val Val Phe Ala Leu Gly Gly Ile Phe Asn Ala Phe Trp
 50 55 60
Leu Met Glu Phe Gly Arg Phe Val Phe Gly Ile Gly Gly Glu Ser Leu
20 65 70 75 80
Ala Val Ala Gln Asn Thr Tyr Ala Val Ser Trp Phe Lys Gly Lys Glu
 85 90 95
Leu Asn Leu Val Phe Gly Leu Gln Leu Ser Met Ala Arg Ile Gly Ser
 100 105 110
25 Thr Val Asn Met Asn Leu Met Gly Trp Leu Tyr Ser Lys Ile Glu Ala

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	115	120	125
	Leu Leu Gly Ser Ala Gly His Thr Thr Leu Gly Ile Thr Leu Met Ile		
	130	135	140
	Gly Gly Ile Thr Cys Ile Leu Ser Leu Ile Cys Ala Leu Ala Leu Ala		
5	145	150	155 160
	Tyr Leu Asp Gln Arg Ala Glu Arg Ile Leu His Lys Glu Gln Gly Lys		
	165	170	175
	Thr Gly Glu Val Ile Lys Leu Thr Asp Val Lys Asp Phe Ser Leu Pro		
	180	185	190
10	Leu Trp Leu Ile Phe Ile Ile Cys Val Cys Tyr Tyr Val Ala Val Phe		
	195	200	205
	Pro Phe Ile Gly Leu Gly Lys Val Phe Phe Thr Glu Lys Phe Gly Phe		
	210	215	220
	Ser Ser Gln Ala Ala Ser Ala Ile Asn Ser Val Val Tyr Val Ile Ser		
15	225	230	235 240
	Ala Pro Met Ser Pro Val Phe Gly Leu Leu Val Asp Lys Thr Gly Lys		
	245	250	255
	Asn Ile Ile Trp Val Leu Cys Ala Val Ala Ala Thr Leu Val Ser His		
	260	265	270
20	Met Met Leu Ala Phe Thr Met Trp Asn Pro Trp Ile Ala Met Cys Leu		
	275	280	285
	Leu Gly Leu Ser Tyr Ser Leu Leu Ala Cys Ala Leu Trp Pro Met Val		
	290	295	300
	Ala Phe Val Val Pro Glu His Gln Leu Gly Thr Ala Tyr Gly Phe Met		
25	305	310	315 320

Gln Ser Ile Gln Asn Leu Gly Leu Ala Ile Ile Ser Ile Ile Ala Gly

330

335

Met Ile Leu Asp Ser Arg Gly Tyr Leu Phe Leu Glu Val Phe Phe Ile

345

350

5 Ala Cys Val Ser Leu Ser Leu Leu Ser Val Val Leu Leu Tyr Leu Val

360

365

Asn Arg Ala Gln Gly Gly Asn Leu Asn Tyr Ser Ala Arg Gln Arg Glu .

375

380

Glu Ile Lys Phe Ser His Thr Glu

385

390

<210> 68

<211> 538

<212> PRT

<213> Homo sapiens

<400> 68

Met Gly Cys Leu Trp Gly Leu Ala Leu Pro Leu Phe Phe Phe Cys Trp

1

5

10

15

Glu Val Gly Val Ser Gly Ser Ser Ala Gly Pro Ser Thr Arg Arg Ala

20

25

30

Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala Met Thr Leu

35

40

45

Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu Ser Ala Glu Thr

50

55

60

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Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Ile Pro Glu Ala Glu Thr
65 70 75 80
Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg Glu Thr Arg Ser Phe Thr
85 90 95
5 Lys Thr Ser Pro Asn Phe Met Val Leu Ile Ala Thr Ser Val Glu Thr
100 105 110
Ser Ala Ala Ser Gly Ser Pro Glu Gly Ala Gly Met Thr Thr Val Gln
115 120 125
Thr Ile Thr Gly Ser Asp Pro Glu Glu Ala Ile Phe Asp Thr Leu Cys
10 130 135 140
Thr Asp Asp Ser Ser Glu Glu Ala Lys Thr Leu Thr Met Asp Ile Leu
145 150 155 160
Thr Leu Ala His Thr Ser Thr Glu Ala Lys Gly Leu Ser Ser Glu Ser
165 170 175
15 Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala
180 185 190
Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro
195 200 205
Ser Arg Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val
20 210 215 220
Ile Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu Ala Glu
225 230 235 240
Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys Ser Ile Thr
245 250 255
25 Glu Ile Glu Thr Thr Thr Ser Ser Ile Pro Gly Ala Ser Asp Ile Asp

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	260	265	270
	Leu Ile Pro Thr Glu Gly Val Lys Ala Ser Ser Thr Ser Asp Pro Pro		
	275	280	285
	Ala Leu Pro Asp Ser Thr Glu Ala Lys Pro His Ile Thr Glu Val Thr		
5	290	295	300
	Ala Ser Ala Glu Thr Leu Ser Thr Ala Gly Thr Thr Glu Ser Ala Ala		
	305	310	315 320
	Pro His Ala Thr Val Gly Thr Pro Leu Pro Thr Asn Ser Ala Thr Glu		
	325	330	335
10	Arg Glu Val Thr Ala Pro Gly Ala Thr Thr Leu Ser Gly Ala Leu Val		
	340	345	350
	Thr Val Ser Arg Asn Pro Leu Glu Glu Thr Ser Ala Leu Ser Val Glu		
	355	360	365
	Thr Pro Ser Tyr Val Lys Val Ser Gly Ala Ala Pro Val Ser Ile Glu		
15	370	375	380
	Ala Gly Ser Ala Val Gly Lys Thr Thr Ser Phe Ala Gly Ser Ser Ala		
	385	390	395 400
	Ser Ser Tyr Ser Pro Ser Glu Ala Ala Leu Lys Asn Phe Thr Pro Ser		
	405	410	415
20	Glu Thr Pro Thr Met Asp Ile Ala Thr Lys Gly Pro Phe Pro Thr Ser		
	420	425	430
	Arg Asp Pro Leu Pro Ser Val Pro Pro Thr Thr Thr Asn Ser Ser Arg		
	435	440	445
	Gly Thr Asn Ser Thr Leu Ala Lys Ile Thr Thr Ser Ala Lys Thr Thr		
25	450	455	460

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Met Lys Pro Pro Thr Ala Thr Pro Thr Thr Ala Arg Thr Arg Pro Thr
 465 470 475 480
 Thr Asp Val Ser Ala Gly Glu Asn Gly Gly Phe Leu Leu Leu Arg Leu
 485 490 495
 5 Ser Val Ala Ser Pro Glu Asp Leu Thr Asp Pro Arg Val Ala Glu Arg
 500 505 510
 Leu Met Gln Gln Leu His Arg Glu Leu His Ala His Ala Pro His Phe
 515 520 525
 Gln Val Ser Leu Leu Arg Val Arg Arg Gly
 10 530 535

 <210> 69
 <211> 102
 <212> PRT
 15 <213> Homo sapiens

 <400> 69
 Met Glu Ala Ala Leu Leu Gly Leu Cys Asn Trp Ser Thr Leu Gly Val
 1 5 10 15
 20 Cys Ala Ala Leu Lys Leu Pro Gln Ile Ser Ala Val Leu Ala Ala Arg
 20 25 30
 Ser Ala Arg Gly Leu Ser Leu Pro Ser Leu Leu Leu Glu Leu Ala Gly
 35 40 45
 Phe Leu Val Phe Leu Arg Tyr Gln Cys Tyr Tyr Gly Tyr Pro Pro Leu
 25 50 55 60

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Thr Tyr Leu Glu Tyr Pro Ile Leu Ile Ala Gln Asp Val Ile Leu Leu
 65 70 75 80
 Leu Cys Ile Phe His Phe Asn Gly Asn Val Lys Gln Ala Thr Pro Tyr
 85 90 95
 5 Ile Ala Val Tyr Pro Phe
 100

 <210> 70
 <211> 442
 10 <212> PRT
 <213> Homo sapiens

 <400> 70
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 Ser Ser Arg Gly Cys Trp Tyr Tyr Leu Arg Tyr Phe Phe Leu Phe Val
 20 25 30
 Ser Leu Ile Gln Phe Leu Ile Ile Leu Gly Leu Val Leu Phe Met Val
 35 40 45
 20 Tyr Gly Asn Val His Val Ser Thr Glu Ser Asn Leu Gln Ala Thr Glu
 50 55 60
 Arg Arg Ala Glu Gly Leu Tyr Ser Gln Leu Leu Gly Leu Thr Ala Ser
 65 70 75 80
 Gln Ser Asn Leu Thr Lys Glu Leu Asn Phe Thr Thr Arg Ala Lys Asp
 25 85 90 95

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Ala Ile Met Gln Met Trp Leu Asn Ala Arg Arg Asp Leu Asp Arg Ile
 100 105 110
 Asn Ala Ser Phe Arg Gln Cys Gln Gly Asp Arg Val Ile Tyr Thr Asn
 115 120 125
 5 Asn Gln Arg Tyr Met Ala Ala Ile Ile Leu Ser Glu Lys Gln Cys Arg
 130 135 140
 Asp Gln Phe Lys Asp Met Asn Lys Ser Cys Asp Ala Leu Leu Phe Met
 145 150 155 160
 Leu Asn Gln Lys Val Lys Thr Leu Glu Val Glu Ile Ala Lys Glu Lys
 10 165 170 175
 Thr Ile Cys Thr Lys Asp Lys Glu Ser Val Leu Leu Asn Lys Arg Val
 180 185 190
 Ala Glu Glu Gln Leu Val Glu Cys Val Lys Thr Arg Glu Leu Gln His
 195 200 205
 15 Gln Glu Arg Gln Leu Ala Lys Glu Gln Leu Gln Lys Val Gln Ala Leu
 210 215 220
 Cys Leu Pro Leu Asp Lys Asp Lys Phe Glu Met Asp Leu Arg Asn Leu
 225 230 235 240
 Trp Arg Asp Ser Ile Ile Pro Arg Ser Leu Asp Asn Leu Gly Tyr Asn
 20 245 250 255
 Leu Tyr His Pro Leu Gly Ser Glu Leu Ala Ser Ile Arg Arg Ala Cys
 260 265 270
 Asp His Met Pro Ser Leu Met Ser Ser Lys Val Glu Glu Leu Ala Arg
 275 280 285
 25 Ser Leu Arg Ala Asp Ile Glu Arg Val Ala Arg Glu Asn Ser Asp Leu

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290 295 300
Gln Arg Gln Lys Leu Glu Ala Gln Gln Gly Leu Arg Ala Ser Gln Glu
305 310 315 320
Ala Lys Gln Lys Val Glu Lys Glu Ala Gln Ala Arg Glu Ala Lys Leu
5 325 330 335
Gln Ala Glu Cys Ser Arg Gln Thr Gln Leu Ala Leu Glu Glu Lys Ala
340 345 350
Val Leu Arg Lys Glu Arg Asp Asn Leu Ala Lys Glu Leu Glu Glu Lys
355 360 365
10 Lys Arg Glu Ala Glu Gln Leu Arg Met Glu Leu Ala Ile Arg Asn Ser
370 375 380
Ala Leu Asp Thr Cys Ile Lys Thr Lys Ser Gln Pro Met Met Pro Val
385 390 395 400
Ser Arg Pro Met Gly Pro Val Pro Asn Pro Gln Pro Ile Asp Pro Ala
15 405 410 415
Ser Leu Glu Glu Phe Lys Arg Lys Ile Leu Glu Ser Gln Arg Pro Pro
420 425 430
Ala Gly Ile Pro Val Ala Pro Ser Ser Gly
435 440
20
<210> 71
<211> 1800
<212> DNA
<213> Homo sapiens

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<400> 71

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gacacagacc cctggaccct ccctcagctg aaggacacaa gccagccctg gaaagagctc 180
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atcgtgggtca gcatgggtggc tgctaagctg ctgactgtcc ggggtgtctgt gccatcatc 480
10 atgggtgtca acgtaggcac atccatcacc agcaccctgg tctcaatggc gcagtcaggg 540
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5 ccctgggacc gcctggtgac ccgtgctgc ccctgcaacg tctgcagccc cccgaaggcc 1740
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<210> 72

<211> 246

10 <212> DNA

<213> Homo sapiens

<400> 72

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ttgggcattc tcattgtccg gtgcttccgg attcttttgg atccatatcg aagcatgccca 180
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gcttag 246

20 <210> 73

<211> 1965

<212> DNA

<213> Homo sapiens

25 <400> 73

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ctagacgggg ccccgttccg ctatgtgtct ggcagcctgc actactttcg ggtaccgagg 180
gtgctttggg ccgaccggct tttgaagatg cgatggagcg gcctcaacgc catacagttt 240
5 tatgtgccct ggaactacca cgagccacag cctggggtct ataactttaa tggcagccgg 300
gacctcattg cttttctgaa tgaggcagct ctacggaacc tgttggtcat actgagacca 360
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10 attcaggtgg agaatgaata tggtagctac agagcctgtg acttcagcta catgaggcac 600
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gcctatgtga tgggtgatgg ggtgttccag ggtgttgtgg agcgaaatat gagagacaaa 1380
ctatttttga cggggaaact ggggtccaaa ctggatatct tgggtggagaa catggggagg 1440
25 ctgagctttg ggtctaacag cagtgaattc aagggcctgt tgaagccacc aattctgggg 1500

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<211> 1173
<212> DNA
<213> Homo sapiens

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atcagcagct gggccacaag tattcctttt ctttgtgtga ctatgggact tctacccggt 180
ttgggttctg ctttcttata ccaagtggct gctgtggtaa ctaccaaata cttcaaaaaa 240
20 cgattggctc tttctacagc tattgcccg tctgggatgg gactgacttt tcttttggca 300
ccctttacaa aattcctgat agatctgtat gactggacag gagcccttat attatttggga 360
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gagaacaatt ctggtattaa agataaaggc agcagtttgt ctgcacatgg tccagaggca 480
catgcaacag aaacacactg ccatgagaca gaagagtcta ccatcaagga cagtactacg 540
25 cagaaggctg gactacctag caaaaattta acagtctcac aaaatcaaag tgaagagttc 600

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atatttactt ggtcttttct cctcagtcag ttagcatact tcatccctac ctttcacctg 780
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gtaaacaggt ttttgggact tgccagtttc tttgctggga tggctgtcct ttctggacca 1140
10 cctatagcag gtaacacctt caccacattc tga 1173

<210> 75

<211> 1359

<212> DNA

15 <213> Homo sapiens

<400> 75

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20 gattatgtga cggtcgcgaa ggatgcctac atgttctggt ggctctatta tgccaccaac 180
tcctgcaaga acttctcaga actgcccctg gtcatgtggc ttcagggcgg tccaggcggg 240
tctagcactg gatttggaac ctttgaggaa attgggcccc ttgacagtga tctcaaacca 300
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gggttcagtt atgtgaatgg tagtggtgcc tatgccaaag acctggctat ggtggcttca 420
25 gacatgatgg ttctoctgaa gacctcttc agttgccaca aagaattcca gacagttcca 480

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5 gtaaataagg ggctctacag agaggccaca gagctgtggg ggaaagcaga aatgatcatt 780
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<210> 76

<211> 1473

<212> DNA

20 <213> Homo sapiens

<400> 76

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25 caccacgcta ccatgaagcg gcaggcggcc gaggaggcct gcatcctgcg aggtggggcg 180

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ctcagcaccg tgcgtgcggg cgccgagctg cgcgctgtgc tcgcgctcct gcgggcaggc 240
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<210> 77

25 <211> 1179

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<212> DNA

<213> Homo sapiens

<400> 77

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173/346

<210> 78

<211> 1617

<212> DNA

<213> Homo sapiens

5

<400> 78

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gacacccttt gcaccgatga cagctctgaa gaggcaaaga cactcacaat ggacatattg 480
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20 acaacttcca gcatccctgg ggctcagac atagatctca tccccacgga aggggtgaag 840
gcctcgtcca cctccgatcc accagctctg cctgactcca ctgaagcaaa accacacatc 900
actgagggtc cagcctctgc cgagaccctg tccacagccg gcaccacaga gtcagctgca 960
cctcatgcca cggttgggac cccactcccc actaacagcg ccacagaaag agaagtgaca 1020
gcacccgggg ccacgaccct cagtggagct ctggtcacag ttagcaggaa tccctggaa 1080
25 gaaacctcag ccctctctgt tgagacacca agttacgtca aagtctcagg agcagctccg 1140

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gtctccatag aggctgggtc agcagtgggc aaaacaactt cctttgctgg gagctctgct 1200
tcctcctaca gcccctcgga agccgcctc aagaacttca ccccttcaga gacaccgacc 1260
atggacatcg caaccaaggg gcccttcccc accagcaggg accctcttcc ttctgtccct 1320
ccgactacaa ccaacagcag ccgagggacg aacagcacct tagccaagat cacaacctca 1380
5 gcgaagacca cgatgaagcc cccaacagcc acgcccacga ctgcccggac gaggccgacc 1440
acagacgtga gtgcaggtga aaatggaggt ttctcctcc tgcggtgag tgtggcttcc 1500
ccggaagacc tactgaccc cagagtggca gaaaggctga tgcagcagct ccaccgggaa 1560
ctccacgccc acgcgcctca cttccaggtc tccttactgc gtgtcaggag aggctaa 1617

10 <210> 79
<211> 309
<212> DNA
<213> Homo sapiens

15 <400> 79
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agtttacttc tggagctggc aggattcctg gtgtttctgc ggtaccagtg ttactatggg 180
tatccgccgc tgacctacct ggagtacccc atcctcatcg cgcaagatgt catcctcctg 240
20 ctctgtatct ttcattttaa cgggaacgtg aagcaggcca ctccttacat cgctgtgtat 300
cctttctga 309

<210> 80
<211> 1329
25 <212> DNA

175/346

<213> Homo sapiens

<400> 80

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ctggggctcg tgctcttcat ggtctatggc aacgtgcacg tgagcacaga gtccaacctg 180
caggccaccg agcgccgagc cgagggccta tacagtcagc tcctagggct cagggcctcc 240
cagtccaact tgaccaagga gctcaacttc accacccgcg ccaaggatgc catcatgcag 300
atgtggctga atgctcgccg cgacctggac cgcatcaatg ccagcttccg ccagtgccag 360
10 ggtgaccggg tcatctacac gaacaatcag aggtacatgg ctgccatcat cttgagtga 420
aagcaatgca gagatcaatt caaggacatg aacaagagct gcgatgcctt gctcttcatg 480
ctgaatcaga aggtgaagac gctggaggtg gagatagcca aggagaagac catttgcaact 540
aaggataagg aaagcgtgct gctgaacaaa cgcgtggcgg aggaacagct ggttgaatgc 600
gtgaaaaccc gggagctgca gcaccaagag cgccagctgg ccaaggagca actgcaaaag 660
15 gtgcaagccc tctgcctgcc cctggacaag gacaagtttg agatggacct tcgtaacctg 720
tggagggact ccattatccc acgcagcctg gacaacctgg gttacaacct ctaccatccc 780
ctgggctcgg aattggcctc catccgcaga gcctgcgacc acatgcccag cctcatgagc 840
tccaaggtgg aggagctggc ccggagcctc cgggcggata tcgaacgcgt ggcccgcgag 900
aactcagacc tccaacgcca gaagctggaa gcccagcagg gcctgcgggc cagtcaggag 960
20 gcgaaacaga aggtggagaa ggaggctcag gcccgggagg ccaagctcca agctgaatgc 1020
tcccggcaga ccagctagc gctggaggag aaggcgggtg tgcggaagga acgagacaac 1080
ctggccaagg agctggaaga gaagaagagg gaggcggagc agctcaggat ggagctggcc 1140
atcagaaact cagccctgga cacctgcac aagaccaagt cgagccgat gatgccagt 1200
tcaaggcca tgggccctgt cccaacccc cagcccatcg accagctag cctggaggag 1260
25 ttcaagagga agatcctgga gtcccagagg cccctgcag gcatccctgt agccccatcc 1320

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agtggtga 1329

<210> 81

<211> 2016

5 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

10 <222> (78)..(1877)

<400> 81

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gtccctgccc gaaatcc atg ccg agt tcc ctt ccc ggc agc cag gtc ccc 110

15 Met Pro Ser Ser Leu Pro Gly Ser Gln Val Pro

1 5 10

cac ccc act ctg gac gcg gtt gac cta gtg gaa aag act ctg agg aat 158

His Pro Thr Leu Asp Ala Val Asp Leu Val Glu Lys Thr Leu Arg Asn

15 20 25

20 gaa ggg acc tcc agt tct gct cca gtc ttg gag gaa ggg gac aca gac 206

Glu Gly Thr Ser Ser Ser Ala Pro Val Leu Glu Glu Gly Asp Thr Asp

30 35 40

ccc tgg acc ctc cct cag ctg aag gac aca agc cag ccc tgg aaa gag 254

Pro Trp Thr Leu Pro Gln Leu Lys Asp Thr Ser Gln Pro Trp Lys Glu

25 45 50 55

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ctc cgc gtg gcc ggc agg ctg cgc cgc gtg gcc ggc agc gtc ctc aag 302
 Leu Arg Val Ala Gly Arg Leu Arg Arg Val Ala Gly Ser Val Leu Lys
 60 65 70 75
 gcc tgc ggg ctc ctc ggc agc ctg tac ttc ttc atc tgc tct ctg gac 350
 5 Ala Cys Gly Leu Leu Gly Ser Leu Tyr Phe Phe Ile Cys Ser Leu Asp
 80 85 90
 gtc ctc agc tcc gcc ttc cag ctg ctg ggc agc aaa gtg gcc gga gac 398
 Val Leu Ser Ser Ala Phe Gln Leu Leu Gly Ser Lys Val Ala Gly Asp
 95 100 105
 10 atc ttc aag gac aac gtg gtg ctg tcc aac cct gtg gct gga ctg gtc 446
 Ile Phe Lys Asp Asn Val Val Leu Ser Asn Pro Val Ala Gly Leu Val
 110 115 120
 att ggc gtg ctg gtc aca gcc ctg gtg cag agt tcc agc acg tcc tcc 494
 Ile Gly Val Leu Val Thr Ala Leu Val Gln Ser Ser Ser Thr Ser Ser
 15 125 130 135
 tcc atc gtg gtc agc atg gtg gct gct aag ctg ctg act gtc cgg gtg 542
 Ser Ile Val Val Ser Met Val Ala Ala Lys Leu Leu Thr Val Arg Val
 140 145 150 155
 tct gtg ccc atc atc atg ggt gtc aac gta ggc aca tcc atc acc agc 590
 20 Ser Val Pro Ile Ile Met Gly Val Asn Val Gly Thr Ser Ile Thr Ser
 160 165 170
 acc ctg gtc tca atg gcg cag tca ggg gac cgg gat gaa ttt cag agg 638
 Thr Leu Val Ser Met Ala Gln Ser Gly Asp Arg Asp Glu Phe Gln Arg
 175 180 185
 25 gct ttc agc ggc tcg gcg gtg cac ggg atc ttc aac tgg ctc aca gtg 686

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Ala Phe Ser Gly Ser Ala Val His Gly Ile Phe Asn Trp Leu Thr Val
190 195 200
ctg gtc ctg ctg cca ctg gag agc gcc acg gcc ctg ctg gag agg cta 734
Leu Val Leu Leu Pro Leu Glu Ser Ala Thr Ala Leu Leu Glu Arg Leu
5 205 210 215
agt gag cta gcc ctg ggt gcc gcc agc ctg aca ccc agg gcg cag gcg 782
Ser Glu Leu Ala Leu Gly Ala Ala Ser Leu Thr Pro Arg Ala Gln Ala
220 225 230 235
ccc gac atc ctc aag gtg ctg acg aag ccg ctc aca cac ctc atc gtg 830
10 Pro Asp Ile Leu Lys Val Leu Thr Lys Pro Leu Thr His Leu Ile Val
240 245 250
cag ctg gac tcc gac atg atc atg agc agt gcc aca ggc aac gcc act 878
Gln Leu Asp Ser Asp Met Ile Met Ser Ser Ala Thr Gly Asn Ala Thr
255 260 265
15 aac agc agt ctc att aag cac tgg tgc ggc acc acg ggg cag ccg acc 926
Asn Ser Ser Leu Ile Lys His Trp Cys Gly Thr Thr Gly Gln Pro Thr
270 275 280
cag gag aac agc agc tgt ggc gcc ttc ggc ccg tgc aca gag aag aac 974
Gln Glu Asn Ser Ser Cys Gly Ala Phe Gly Pro Cys Thr Glu Lys Asn
20 285 290 295
agc aca gcc ccg gcg gac agg ctg ccc tgc cgc cac ctg ttt gcg ggc 1022
Ser Thr Ala Pro Ala Asp Arg Leu Pro Cys Arg His Leu Phe Ala Gly
300 305 310 315
acg gag ctc acg gac ctg gcc gtg ggc tgc atc ctg ctg gcc ggc tcc 1070
25 Thr Glu Leu Thr Asp Leu Ala Val Gly Cys Ile Leu Leu Ala Gly Ser

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	320	325	330	
	ctg ctg gtg ctc tgc ggc tgc ctg gtc ctc ata gtc aag ctg ctc aac			1118
	Leu Leu Val Leu Cys Gly Cys Leu Val Leu Ile Val Lys Leu Leu Asn			
	335	340	345	
5	tct gtg ctg cgc ggc cgc gtg gcc cag gtc gtg agg aca gtc atc aat			1166
	Ser Val Leu Arg Gly Arg Val Ala Gln Val Val Arg Thr Val Ile Asn			
	350	355	360	
	gcg gac ttc ccc ttc ccg ctg ggc tgg ctc ggc ggc tac ctg gcc gtc			1214
	Ala Asp Phe Pro Phe Pro Leu Gly Trp Leu Gly Gly Tyr Leu Ala Val			
10	365	370	375	
	ctc gcg ggc gcc ggc ctg acc ttc gca ctg cag agc agc agc gtc ttc			1262
	Leu Ala Gly Ala Gly Leu Thr Phe Ala Leu Gln Ser Ser Ser Val Phe			
	380	385	390	395
	acg gcg gcc gtc gtg ccc ctc atg ggg gtc ggg gtg atc agt ctg gac			1310
15	Thr Ala Ala Val Val Pro Leu Met Gly Val Gly Val Ile Ser Leu Asp			
	400	405	410	
	cgg gcg tac ccc ctc tta ctg ggc tcc aac atc ggc acc act acc aca			1358
	Arg Ala Tyr Pro Leu Leu Leu Gly Ser Asn Ile Gly Thr Thr Thr Thr			
	415	420	425	
20	gcc ctg ctg gct gcc ctg gcc agc ccc gca gac agg atg ctc agc gcc			1406
	Ala Leu Leu Ala Ala Leu Ala Ser Pro Ala Asp Arg Met Leu Ser Ala			
	430	435	440	
	ctg cag gtc gcc ctc atc cac ttc ttc ttc aac ctg gcc ggc atc ctg			1454
	Leu Gln Val Ala Leu Ile His Phe Phe Phe Asn Leu Ala Gly Ile Leu			
25	445	450	455	

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	ctg tgg tac ctg gtg cct gca ctg cgg ctg ccc atc ccg ctg gcc agg	1502
	Leu Trp Tyr Leu Val Pro Ala Leu Arg Leu Pro Ile Pro Leu Ala Arg	
	460 465 470 475	
	cac ttc ggg gtg gtg acc gcc cgt tac cgc tgg gtg gct ggg gtc tac	1550
5	His Phe Gly Val Val Thr Ala Arg Tyr Arg Trp Val Ala Gly Val Tyr	
	480 485 490	
	ctg ctg ctc gga ttc ctg ctg ctg ccc ctg gcg gcc ttc ggg ctc tcc	1598
	Leu Leu Leu Gly Phe Leu Leu Leu Pro Leu Ala Ala Phe Gly Leu Ser	
	495 500 505	
10	ctg gca ggg ggc atg gtg ctg gcc gct gtc ggg ggt ccc ctg gtg ggg	1646
	Leu Ala Gly Gly Met Val Leu Ala Ala Val Gly Gly Pro Leu Val Gly	
	510 515 520	
	ctg gtg ctc ctc gtc atc ctg gtt act gtc ctg cag cgg cgc cgg ccg	1694
	Leu Val Leu Leu Val Ile Leu Val Thr Val Leu Gln Arg Arg Arg Pro	
15	525 530 535	
	gcc tgg ctg cct gtc cgc ctg cgc tcc tgg gcc tgg ctc ccc gtc tgg	1742
	Ala Trp Leu Pro Val Arg Leu Arg Ser Trp Ala Trp Leu Pro Val Trp	
	540 545 550 555	
	ctc cat tct ctg gag ccc tgg gac cgc ctg gtg acc cgc tgc tgc ccc	1790
20	Leu His Ser Leu Glu Pro Trp Asp Arg Leu Val Thr Arg Cys Cys Pro	
	560 565 570	
	tgc aac gtc tgc agc ccc ccg aag gcc acc acc aaa gag gcc tac tgc	1838
	Cys Asn Val Cys Ser Pro Pro Lys Ala Thr Thr Lys Glu Ala Tyr Cys	
	575 580 585	
25	tac gag aac cct gag atc ttg gcc tcc cag cag ttg tga cgggcagttg	1887

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Tyr Glu Asn Pro Glu Ile Leu Ala Ser Gln Gln Leu

590

595

600

ctgcgcagac cgccccaccc tccccggctg ggagggctct ggagggccct ggaggggggg 1947

tccccgcggc agctgacctc cggtcacctg ctcccccttc tgtgcaaata aaccaggctg 2007

5 ttatctggg 2016

<210> 82

<211> 1446

<212> DNA

<213> Homo sapiens

10

<220>

<221> CDS

<222> (337) .. (582)

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gctgggcttc tattaaaatt agactctatt tcctgagcac ccacaaatgg acctgacaaa 180

gggaagacac agatgtactg cgtgatgagg aaagcctatc aggattaata tatggctata 240

20 actcagcctc tccagagtgc agccaccatg acctccgcag attgatgatg gaagaaaaga 300

aaaccaggat atcctgtgct ctggcttccc tggacc atg gat gga gga cag ccc 354

Met Asp Gly Gly Gln Pro

1

5

atc ccc tca tcc cta gtg ccc ctt ggg aac gaa tca gca gat tct agc 402

25 Ile Pro Ser Ser Leu Val Pro Leu Gly Asn Glu Ser Ala Asp Ser Ser

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	10	15	20	
	atg tcc ctg gag cag aaa atg aca ttt gtt ttt gtg att ctg ttg ttt			450
	Met Ser Leu Glu Gln Lys Met Thr Phe Val Phe Val Ile Leu Leu Phe			
	25	30	35	
5	att ttc ttg ggc att ctc att gtc cgg tgc ttc cgg att ctt ttg gat			498
	Ile Phe Leu Gly Ile Leu Ile Val Arg Cys Phe Arg Ile Leu Leu Asp			
	40	45	50	
	cca tat cga agc atg cca acc tct acc tgg gct gat gga ctt gaa ggc			546
	Pro Tyr Arg Ser Met Pro Thr Ser Thr Trp Ala Asp Gly Leu Glu Gly			
10	55	60	65	70
	ctg gag aaa ggg cag ttc gac cat gcc ctt gct tag gagggatggt			592
	Leu Glu Lys Gly Gln Phe Asp His Ala Leu Ala			
	75	80		
	gtgggatctc ctcttgagga gatgaagtgc tttgtgtctt ggtgaggatt ccctttatatt			652
15	agtgtttctca acaaatcaaa tttaaacaat atttgggtccc aggaccataa tccattattc			712
	cataaatatg cagttgggtt aaagacattt gaggatgttg gaaatggaca cttatataac			772
	taatccaaca taagaagggt taaattttta tgtttgctca atgaatgagt actcttaaaa			832
	ttgtgtgatt gtgaaaccaa gagcgttaat actgacatag atttgccatc aaacaaaaca			892
	ccacctgac tgactaaaga ataaaagact agaaaggatc tcatatgaat ctggtgacaa			952
20	ggccaggaag agatttcctt gctctaatta tgtctatatt tgttttattt catgggcacc			1012
	tatctgggtc ctgagcagaa tgaggaagat tgtgctgaat ggacccaaag tagtttcttg			1072
	ttttctccca aagcaggag ctttgggaag caatggaaaa gcttaaaaga gatgattctg			1132
	tccttggtaa atgtgagtga gaatagcgtt ttgtttttca agtaaaactt aattcaaagg			1192
	ctacaaagtt ttaaaaacta tttaccaagc caactacatt atatgtattc atattaataa			1252
25	catgtgtaga ggtagctata cattacttga atttacactt tacacaaatg atttaaaaaa			1312

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taggttgcaa gtgcagctta aagttttttt tcaatgaaaa gttaattggt tagaggagaa 1372
 gacttttata gtcttcagag gaatgtgtat ttatgattgt atatagtcac caaataaaac 1432
 ttttcaagaa acag 1446

5 <210> 83
 <211> 2467
 <212> DNA
 <213> Homo sapiens

10 <220>
 <221> CDS
 <222> (40)..(2004)

<400> 83

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 Met Ala Pro Lys Lys
 1 5

ctg tcc tgc ctt cgt tcc ctg ctg ctg ccg ctc agc ctg acg cta ctg 102
 Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu Ser Leu Thr Leu Leu

20 10 15 20
 ctg ccc cag gca gac act cgg tcg ttc gta gtg gat agg ggt cat gac 150
 Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val Asp Arg Gly His Asp

25 25 30 35
 cgg ttt ctc cta gac ggg gcc ccg ttc cgc tat gtg tct ggc agc ctg 198
 Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr Val Ser Gly Ser Leu

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	40	45	50	
	cac tac ttt.cgg gta ccg cgg gtg ctt tgg gcc gac cgg ctt ttg aag	246		
	His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala Asp Arg Leu Leu Lys			
	55	60	65	
5	atg cga tgg agc ggc ctc aac gcc ata cag ttt tat gtg ccc tgg aac	294		
	Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe Tyr Val Pro Trp Asn			
	70	75	80	85
	tac cac gag cca cag cct ggg gtc tat aac ttt aat ggc agc cgg gac	342		
	Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe Asn Gly Ser Arg Asp			
10	90	95	100	
	ctc att gcc ttt ctg aat gag gca gct cta gcg aac ctg ttg gtc ata	390		
	Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala Asn Leu Leu Val Ile			
	105	110	115	
	ctg aga cca gga cct tac atc tgt gca gag tgg gag atg ggg ggt ctc	438		
15	Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp Glu Met Gly Gly Leu			
	120	125	130	
	cca tcc tgg ttg ctt cga aaa cct gaa att cat cta aga acc tca gat	486		
	Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His Leu Arg Thr Ser Asp			
	135	140	145	
20	cca gac ttc ctt gcc gca gtg gac tcc tgg ttc aag gtc ttg ctg ccc	534		
	Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe Lys Val Leu Leu Pro			
	150	155	160	165
	aag ata tat cca tgg ctt tat cac aat ggg ggc aac atc att agc att	582		
	Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly Asn Ile Ile Ser Ile			
25	170	175	180	

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	cag gtg gag aat gaa tat ggt agc tac aga gcc tgt gac ttc agc tac	630
	Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala Cys Asp Phe Ser Tyr	
	185 190 195	
	atg agg cac ttg gct ggg ctc ttc cgt gca ctg cta gga gaa aag atc	678
5	Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu Leu Gly Glu Lys Ile	
	200 205 210	
	ttg ctc ttc acc aca gat ggg cct gaa gga ctc aag tgt ggc tcc ctc	726
	Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu Lys Cys Gly Ser Leu	
	215 220 225	
10	cgg gga ctc tat acc act gta gat ttt ggc cca gct gac aac atg acc	774
	Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro Ala Asp Asn Met Thr	
	230 235 240 245	
	aaa atc ttt acc ctg ctt cgg aag tat gaa ccc cat ggg cca ttg gta	822
	Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro His Gly Pro Leu Val	
15	250 255 260	
	aac tct gag tac tac aca ggc tgg ctg gat tac tgg ggc cag aat cac	870
	Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr Trp Gly Gln Asn His	
	265 270 275	
	tcc aca cgg tct gtg tca gct gta acc aaa gga cta gag aac atg ctc	918
20	Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly Leu Glu Asn Met Leu	
	280 285 290	
	aag ttg gga gcc agt gtg aac atg tac atg ttc cat gga ggt acc aac	966
	Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe His Gly Gly Thr Asn	
	295 300 305	
25	ttt gga tat tgg aat ggt gcc gat aag aag gga cgc ttc ctt ccg att	1014

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	Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly Arg Phe Leu Pro Ile	
	310 315 320 325	
	act acc agc tat gac tat gat gca cct ata tct gaa gca ggg gac ccc	1062
	Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser Glu Ala Gly Asp Pro	
5	330 335 340	
	aca cct aag ctt ttt gct ctt cga gat gtc atc agc aag ttc cag gaa	1110
	Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile Ser Lys Phe Gln Glu	
	345 350 355	
	gtt cct ttg gga cct tta cct ccc ccg agc ccc aag atg atg ctt gga	1158
10	Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro Lys Met Met Leu Gly	
	360 365 370	
	cct gtg act ctg cac ctg gtt ggg cat tta ctg gct ttc cta gac ttg	1206
	Pro Val Thr Leu His Leu Val Gly His Leu Leu Ala Phe Leu Asp Leu	
	375 380 385	
15	ctt tgc ccc cgt ggg ccc att cat tca atc ttg cca atg acc ttt gag	1254
	Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu Pro Met Thr Phe Glu	
	390 395 400 405	
	gct gtc aag cag gac cat ggc ttc atg ttg tac cga acc tat atg acc	1302
	Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr Arg Thr Tyr Met Thr	
20	410 415 420	
	cat acc att ttt gag cca aca cca ttc tgg gtg cca aat aat gga gtc	1350
	His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val Pro Asn Asn Gly Val	
	425 430 435	
	cat gac cgt gcc tat gtg atg gtg gat ggg gtg ttc cag ggt gtt gtg	1398
25	His Asp Arg Ala Tyr Val Met Val Asp Gly Val Phe Gln Gly Val Val	

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	440	445	450	
	gag cga aat atg aga gac aaa cta ttt ttg acg ggg aaa ctg ggg tcc			1446
	Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr Gly Lys Leu Gly Ser			
	455	460	465	
5	aaa ctg gat atc ttg gtg gag aac atg ggg agg ctc agc ttt ggg tct			1494
	Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg Leu Ser Phe Gly Ser			
	470	475	480	485
	aac agc agt gac ttc aag ggc ctg ttg aag cca cca att ctg ggg caa			1542
	Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro Pro Ile Leu Gly Gln			
10	490	495	500	
	aca atc ctt acc cag tgg atg atg ttc cct ctg aaa att gat aac ctt			1590
	Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu Lys Ile Asp Asn Leu			
	505	510	515	
	gtg aag tgg tgg ttt ccc ctc cag ttg cca aaa tgg cca tat cct caa			1638
15	Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys Trp Pro Tyr Pro Gln			
	520	525	530	
	gct cct tct ggc ccc aca ttc tac tcc aaa aca ttt cca att tta ggc			1686
	Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr Phe Pro Ile Leu Gly			
	535	540	545	
20	tca gtt ggg gac aca ttt cta tat cta cct gga tgg acc aag ggc caa			1734
	Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly Trp Thr Lys Gly Gln			
	550	555	560	565
	gtc tgg atc aat ggg ttt aac ttg ggc cgg tac tgg aca aag cag ggg			1782
	Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr Trp Thr Lys Gln Gly			
25	570	575	580	

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cca caa cag acc ctc tac gtg cca aga ttc ctg ctg ttt cct agg gga 1830
 Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu Leu Phe Pro Arg Gly
 585 590 595

gcc ctc aac aaa att aca ttg ctg gaa cta gaa gat gta cct ctc cag 1878
 5 Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu Asp Val Pro Leu Gln
 600 605 610

ccc caa gtc caa ttt ttg gat aag cct atc ctc aat agc act agt act 1926
 Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu Asn Ser Thr Ser Thr
 615 620 625

10 ttg cac agg aca cat atc aat tcc ctt tca gct gat aca ctg agt gcc 1974
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 630 635 640 645

tct gaa cca atg gag tta agt ggg cac tga aaggtaggcc gggcatgggtg 2024
 Ser Glu Pro Met Glu Leu Ser Gly His

15 650 655

gctcatgcct gtaatcccag cactttggga ggctgagacg ggtggattac ctgaggtcag 2084
 gacttcaaga ccagcctggc caacatgggtg aaaccccgtc tccactaaaa atacaaaaat 2144
 tagccgggcg tgatgggtggg cacctctaata cccagctact tgggagggtg agggcaggag 2204
 aattgcttga atccaggagg cagaggttgc agtgagtgga ggttgtacca ctgcactcca 2264

20 gcctggctga cagtgagaca ctccatctca aaaaaaaaaa aaaaaaaaaa aagtaaccct 2324
 tggacctggg acatggagtg ggcaggatcc cttggtgctg gccacggtga ccctaaggaa 2384
 ctaaaggcca cagtgcctct gaatgtaagt acaagtacac attccttgcc aaactttatt 2444
 gtgattaataa ttccagagac agt 2467

25 <210> 84

189/346

<211> 1450

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<213> Homo sapiens

5 <220>

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<400> 84

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 catctgtgga ggatttcttt gctgaacacc acatcaaagg gatcttctgc atttaaaata 180
 gaagaggcat catgctgaag agggagggga aggtccaacc ttacactaaa accctggatg 240
 gagg atg ggg atg gat gat tgt gat tca ttt ttt cct ggt ccc ctg gtt 289

15 Met Gly Met Asp Asp Cys Asp Ser Phe Phe Pro Gly Pro Leu Val
 1 5 10 15

 gct att att tgt gac ata ctt gga gag aaa act acc tcc att ctt ggg 337
 Ala Ile Ile Cys Asp Ile Leu Gly Glu Lys Thr Thr Ser Ile Leu Gly

 20 25 30

20 gct ttt gtt gtt act ggt gga tat ctg atc agc agc tgg gcc aca agt 385
 Ala Phe Val Val Thr Gly Gly Tyr Leu Ile Ser Ser Trp Ala Thr Ser

 35 40 45

 att cct ttt ctt tgt gtg act atg gga ctt cta ccc ggt ttg ggt tct 433
 Ile Pro Phe Leu Cys Val Thr Met Gly Leu Leu Pro Gly Leu Gly Ser

25 50 55 60

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gct ttc tta tac caa gtg gct gct gtg gta act acc aaa tac ttc aaa 481
 Ala Phe Leu Tyr Gln Val Ala Ala Val Val Thr Thr Lys Tyr Phe Lys
 65 70 75
 aaa cga ttg gct ctt tct aca gct att gcc cgt tct ggg atg gga ctg 529
 5 Lys Arg Leu Ala Leu Ser Thr Ala Ile Ala Arg Ser Gly Met Gly Leu
 80 85 90 95
 act ttt ctt ttg gca ccc ttt aca aaa ttc ctg ata gat ctg tat gac 577
 Thr Phe Leu Leu Ala Pro Phe Thr Lys Phe Leu Ile Asp Leu Tyr Asp
 100 105 110
 10 tgg aca gga gcc ctt ata tta ttt gga gct atc gca ttg aat ttg gtg 625
 Trp Thr Gly Ala Leu Ile Leu Phe Gly Ala Ile Ala Leu Asn Leu Val
 115 120 125
 cct tct agt atg ctc tta aga ccc atc cat atc aaa agt gag aac aat 673
 Pro Ser Ser Met Leu Leu Arg Pro Ile His Ile Lys Ser Glu Asn Asn
 15 130 135 140
 tct ggt att aaa gat aaa ggc agc agt ttg tct gca cat ggt cca gag 721
 Ser Gly Ile Lys Asp Lys Gly Ser Ser Leu Ser Ala His Gly Pro Glu
 145 150 155
 gca cat gca aca gaa aca cac tgc cat gag aca gaa gag tct acc atc 769
 20 Ala His Ala Thr Glu Thr His Cys His Glu Thr Glu Glu Ser Thr Ile
 160 165 170 175
 aag gac agt act acg cag aag gct gga cta cct agc aaa aat tta aca 817
 Lys Asp Ser Thr Thr Gln Lys Ala Gly Leu Pro Ser Lys Asn Leu Thr
 180 185 190
 25 gtc tca caa aat caa agt gaa gag ttc tac aat ggg cct aac agg aac 865

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	Val Ser Gln Asn Gln Ser Glu Glu Phe Tyr Asn Gly Pro Asn Arg Asn	
	195	200 205
	aga ctg tta tta aag agt gat gaa gaa agt gat aag gtt att tcg tgg	913
	Arg Leu Leu Leu Lys Ser Asp Glu Glu Ser Asp Lys Val Ile Ser Trp	
5	210 215 220	
	agc tgc aaa caa ctg ttt gac att tct ctc ttt aga aat cct ttc ttc	961
	Ser Cys Lys Gln Leu Phe Asp Ile Ser Leu Phe Arg Asn Pro Phe Phe	
	225 230 235	
	tac ata ttt act tgg tct ttt ctc ctc agt cag tta gca tac ttc atc	1009
10	Tyr Ile Phe Thr Trp Ser Phe Leu Leu Ser Gln Leu Ala Tyr Phe Ile	
	240 245 250 255	
	cct acc ttt cac ctg gta gcc aga gcc aaa aca ctg ggg att gac atc	1057
	Pro Thr Phe His Leu Val Ala Arg Ala Lys Thr Leu Gly Ile Asp Ile	
	260 265 270	
15	atg gat gcc tct tac ctt gtt tct gta gca ggt atc ctt gag acg gtc	1105
	Met Asp Ala Ser Tyr Leu Val Ser Val Ala Gly Ile Leu Glu Thr Val	
	275 280 285	
	agt cag att att tct gga tgg gtt gct gat caa aac tgg att aag aag	1153
	Ser Gln Ile Ile Ser Gly Trp Val Ala Asp Gln Asn Trp Ile Lys Lys	
20	290 295 300	
	tat cat tac cac aag tct tac ctc atc ctc tgc ggc atc act aac ctg	1201
	Tyr His Tyr His Lys Ser Tyr Leu Ile Leu Cys Gly Ile Thr Asn Leu	
	305 310 315	
	ctt gct cct tta gcc acc aca ttt cca cta ctt atg acc tac acc atc	1249
25	Leu Ala Pro Leu Ala Thr Thr Phe Pro Leu Leu Met Thr Tyr Thr Ile	

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320 325 330 335
tgc ttt gcc atc ttt gct ggt ggt tac ctg gca ttg ata ctg cct gta 1297
Cys Phe Ala Ile Phe Ala Gly Gly Tyr Leu Ala Leu Ile Leu Pro Val
340 345 350
5 ctg gtt gat ctg tgt agg aat tct aca gta aac agg ttt ttg gga ctt 1345
Leu Val Asp Leu Cys Arg Asn Ser Thr Val Asn Arg Phe Leu Gly Leu
355 360 365
gcc agt ttc ttt gct ggg atg gct gtc ctt tct gga cca cct ata gca 1393
Ala Ser Phe Phe Ala Gly Met Ala Val Leu Ser Gly Pro Pro Ile Ala
10 370 375 380
ggt aac acc ttc acc aca ttc tga acaaatttca atagcaataa aagagaaaaa 1447
Gly Asn Thr Phe Thr Thr Phe
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ctg 1450
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25 <400> 85

193/346

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 ctg ctg ctg ccg ctg ctg ctg ggc ctg aac gca gga gct gtc att gac 97
 5 Leu Leu Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp
 15 20 25 30
 tgg ccc aca gag gag ggc aag gaa gta tgg gat tat gtg acg gtc cgc 145
 Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val Arg
 35 40 45
 10 aag gat gcc tac atg ttc tgg tgg ctc tat tat gcc acc aac tcc tgc 193
 Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn Ser Cys
 50 55 60
 aag aac ttc tca gaa ctg ccc ctg gtc atg tgg ctt cag ggc ggt cca 241
 Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln Gly Gly Pro
 15 65 70 75
 ggc ggt tct agc act gga ttt gga aac ttt gag gaa att ggg ccc ctt 289
 Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu Ile Gly Pro Leu
 80 85 90
 gac agt gat ctc aaa cca cgg aaa acc acc tgg ctc cag gct gcc agt 337
 20 Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp Leu Gln Ala Ala Ser
 95 100 105 110
 ctc cta ttt gtg gat aat ccc gtg ggc act ggg ttc agt tat gtg aat 385
 Leu Leu Phe Val Asp Asn Pro Val Gly Thr Gly Phe Ser Tyr Val Asn
 115 120 125
 25 ggt agt ggt gcc tat gcc aag gac ctg gct atg gtg gct tca gac atg 433

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Gly Ser Gly Ala Tyr Ala Lys Asp Leu Ala Met Val Ala Ser Asp Met
 130 135 140
 atg gtt ctc ctg aag acc ttc ttc agt tgc cac aaa gaa ttc cag aca 481
 Met Val Leu Leu Lys Thr Phe Phe Ser Cys His Lys Glu Phe Gln Thr
 5 145 150 155
 gtt cca ttc tac att ttc tca gag tcc tat gga gga aaa atg gca gct 529
 Val Pro Phe Tyr Ile Phe Ser Glu Ser Tyr Gly Gly Lys Met Ala Ala
 160 165 170
 ggc att ggt cta gag ctt tat aag gcc att cag cga ggg acc atc aag 577
 10 Gly Ile Gly Leu Glu Leu Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys
 175 180 185 190
 tgc aac ttt gcg ggg gtt gcc ttg ggt gat tcc tgg atc tcc cct gtt 625
 Cys Asn Phe Ala Gly Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val
 195 200 205
 15 gat tcg gtg ctc tcc tgg gga cct tac ctg tac agc atg tct ctt ctc 673
 Asp Ser Val Leu Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu
 210 215 220
 gaa gac aaa ggt ctg gca gag gtg tct aag gtt gca gag caa gta ctg 721
 Glu Asp Lys Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu
 20 225 230 235
 aat gcc gta aat aag ggg ctc tac aga gag gcc aca gag ctg tgg ggg 769
 Asn Ala Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly
 240 245 250
 aaa gca gaa atg atc att gaa cag aac aca gat ggg gtg aac ttc tat 817
 25 Lys Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr

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	255	260	265	270	
	aac atc tta act aaa agc act ccc acg tct aca atg gag tcg agt cta	865			
	Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser Leu				
	275	280	285		
5	gaa ttc aca cag agc cac cta gtt tgt ctt tgt cag cgc cac gtg aga	913			
	Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His Val Arg				
	290	295	300		
	cac cta caa cga gat gcc tta agc cag ctc atg aat ggc ccc atc aga	961			
	His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly Pro Ile Arg				
10	305	310	315		
	aag aag ctc aaa att att cct gag gat caa tcc tgg gga ggc cag gct	1009			
	Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp Gly Gly Gln Ala				
	320	325	330		
	acc aac gtc ttt gtg aac atg gag gag gac ttc atg aag cca gtc att	1057			
15	Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe Met Lys Pro Val Ile				
	335	340	345	350	
	agc att gtg gac gag ttg ctg gag gca ggg atc aac gtg acg gtg tat	1105			
	Ser Ile Val Asp Glu Leu Leu Glu Ala Gly Ile Asn Val Thr Val Tyr				
	355	360	365		
20	aat gga cag ctg gat ctc atc gta gat acc atg ggt cag gag gcc tgg	1153			
	Asn Gly Gln Leu Asp Leu Ile Val Asp Thr Met Gly Gln Glu Ala Trp				
	370	375	380		
	gtg cgg aaa ctg aag tgg cca gaa ctg cct aaa ttc agt cag ctg aag	1201			
	Val Arg Lys Leu Lys Trp Pro Glu Leu Pro Lys Phe Ser Gln Leu Lys				
25	385	390	395		

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tgg aag gcc ctg tac agt gac cct aaa tct ctg gaa aca tct gct ttt 1249
 Trp Lys Ala Leu Tyr Ser Asp Pro Lys Ser Leu Glu Thr Ser Ala Phe
 400 405 410
 gtc aag tcc tac aag aac ctt gct ttc tac tgg att ctg aaa gct ggt 1297
 5 Val Lys Ser Tyr Lys Asn Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly
 415 420 425 430
 cat atg gtt cct tct gac caa ggg gac atg gct ctg aag atg atg aga 1345
 His Met Val Pro Ser Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg
 435 440 445
 10 ctg gtg act cag caa gaa tag gatggatggg gctggagatg agctgggttg 1396
 Leu Val Thr Gln Gln Glu
 450
 gccttggggc acagagctga gctgaggccg ctgaagctgt aggaagcgcc attcttccct 1456
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 15 ttgtctctgg aggcaatttg gaaattatct ctgcttctta aaaaaaccta agatttttta 1576
 aaaaattgat ttgttttgat caaaataaag gatgataata gatattatct tttcttatga 1636
 cagaagcaaa tgatgtgatt tatagaaaaa ctgggaaata caggtagcca aagagtaaata 1696
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 gcagaatctt tttttctata tatacatata ttttttttac caaaatgaat cattactcta 1816
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<210> 86

<211> 1856

25 <212> DNA

197/346

<213> Homo sapiens

<220>

<221> CDS

5 <222> (43)..(1515)

<400> 86

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10                                     1
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Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro Gly Pro Gly Gly
      5              10              15              20
ggc gaa cac ccc act gcc gac cgt gct ggc tgc tcg gcc tcg ggg gcc      150
15 Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser Ala Ser Gly Ala
              25              30              35
tgc tac agc ctg cac cac gct acc atg aag cgg cag gcg gcc gag gag      198
Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln Ala Ala Glu Glu
              40              45              50
20 gcc tgc atc ctg cga ggt ggg gcg ctc agc acc gtg cgt gcg ggc gcc      246
Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val Arg Ala Gly Ala
              55              60              65
gag ctg cgc gct gtg ctc gcg ctc ctg cgg gca ggc cca ggg ccc gga      294
Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly Pro Gly Pro Gly
25              70              75              80

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ggg ggc tcc aaa gac ctg ctg ttc tgg gtc gca ctg gag cgc agg cgt 342
Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu Glu Arg Arg Arg
      85              90              95              100
tcc cac tgc acc ctg gag aac gag cct ttg cgg ggt ttc tcc tgg ctg 390
5  Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly Phe Ser Trp Leu
      105              110              115
tcc tcc gac ccc ggc ggt ctc gaa agc gac acg ctg cag tgg gtg gag 438
Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu Gln Trp Val Glu
      120              125              130
10 gag ccc caa cgc tcc tgc acc gcg cgg aga tgc gcg gta ctc cag gcc 486
Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala Val Leu Gln Ala
      135              140              145
acc ggt ggg gtc gag ccc gca ggc tgg aag gag atg cga tgc cac ctg 534
Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met Arg Cys His Leu
15      150              155              160
cgc gcc aac ggc tac ctg tgc aag tac cag ttt gag gtc ttg tgt cct 582
Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu Val Leu Cys Pro
      165              170              175              180
gcg ccg cgc ccc ggg gcc gcc tct aac ttg agc tat cgc gcg ccc ttc 630
20 Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr Arg Ala Pro Phe
      185              190              195
cag ctg cac agc gcc gct ctg gac ttc agt cca cct ggg acc gag gtg 678
Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro Gly Thr Glu Val
      200              205              210
25 agt gcg ctc tgc cgg gga cag ctc ccg atc tca gtt act tgc atc gcg 726

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Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val Thr Cys Ile Ala
 215 220 225
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 Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly Asp Val Leu Cys
 5 230 235 240
 ccc tgc ccc ggg agg tac ctc cgt gct ggc aaa tgc gca gag ctc cct 822
 Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys Ala Glu Leu Pro
 245 250 255 260
 aac tgc cta gac gac ttg gga ggc ttt gcc tgc gaa tgt gct acg ggc 870
 10 Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu Cys Ala Thr Gly
 265 270 275
 ttc gag ctg ggg aag gac ggc cgc tct tgt gtg acc agt ggg gaa gga 918
 Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr Ser Gly Glu Gly
 280 285 290
 15 cag ccg acc ctt ggg ggg acc ggg gtg ccc acc agg cgc ccg ccg gcc 966
 Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg Arg Pro Pro Ala
 295 300 305
 act gca acc agc ccc gtg ccg cag aga aca tgg cca atc agg gtc gac 1014
 Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro Ile Arg Val Asp
 20 310 315 320
 gag aag ctg gga gag aca cca ctt gtc cct gaa caa gac aat tca gta 1062
 Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln Asp Asn Ser Val
 325 330 335 340
 aca tct att cct gag att cct cga tgg gga tca cag agc acg atg tct 1110
 25 Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln Ser Thr Met Ser

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	345	350	355	
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	Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala Thr Ile Thr Pro			
	360	365	370	
5	tca ggg agc gtg att tcc aag ttt aat tct acg act tcc tct gcc act			1206
	Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr Ser Ser Ala Thr			
	375	380	385	
	cct cag gct ttc gac tcc tcc tct gcc gtg gtc ttc ata ttt gtg agc			1254
	Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe Ile Phe Val Ser			
10	390	395	400	
	aca gca gta gta gtg ttg gtg atc ttg acc atg aca gta ctg ggg ctt			1302
	Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr Val Leu Gly Leu			
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	gtc aag ctc tgc ttt cac gaa agc ccc tct tcc cag cca agg aag gag			1350
15	Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln Pro Arg Lys Glu			
	425	430	435	
	tct atg ggc ccg ccg ggc ctg gag agt gat cct gag ccc gct gct ttg			1398
	Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu Pro Ala Ala Leu			
	440	445	450	
20	ggc tcc agt tct gca cat tgc aca aac aat ggg gtg aaa gtc ggg gac			1446
	Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val Lys Val Gly Asp			
	455	460	465	
	tgt gat ctg cgg gac aga gca gag ggt gcc ttg ctg gcg gag tcc cct			1494
	Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu Ala Glu Ser Pro			
25	470	475	480	

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Leu Gly Ser Ser Asp Ala
485 490
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5 ttctgcagaa atcccccttc ctctaaattc cttttactcc actgaggagc taaatcagaa 1665
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cgcccctgga gccctgccgg ccctctgcga cccagtcgc ctggcgccacc ggcttttgggt 180
gctgttactg atgtgcttcc ttggctttgc tatttttgct atgataatcc tgctgccctt 240
25 cagactcaag ttaaacgaga t atg caa gtg aat acc acg aaa ttc atg ctg 291

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	Met	Gln	Val	Asn	Thr	Thr	Lys	Phe	Met	Leu							
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	Leu	Tyr	Ala	Trp	Tyr	Ser	Trp	Pro	Asn	Val	Val	Leu	Cys	Phe	Phe	Gly	
5			15			20						25					
	ggc	ttt	ttg	ata	gac	cga	gta	ttt	gga	ata	cga	tgg	ggc	aca	atc	att	387
	Gly	Phe	Leu	Ile	Asp	Arg	Val	Phe	Gly	Ile	Arg	Trp	Gly	Thr	Ile	Ile	
			30			35						40					
	ttt	agc	tgc	ttt	gtt	tgc	att	gga	cag	gtt	gtt	ttt	gcc	ctg	ggg	gga	435
10	Phe	Ser	Cys	Phe	Val	Cys	Ile	Gly	Gln	Val	Val	Phe	Ala	Leu	Gly	Gly	
			45			50						55					
	ata	ttt	aat	gct	ttt	tgg	ctg	atg	gaa	ttt	gga	aga	ttt	gta	ttt	ggg	483
	Ile	Phe	Asn	Ala	Phe	Trp	Leu	Met	Glu	Phe	Gly	Arg	Phe	Val	Phe	Gly	
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15	att	ggg	ggc	gag	tcc	tta	gca	gtt	gcc	cag	aat	aca	tat	gct	gtg	agc	531
	Ile	Gly	Gly	Glu	Ser	Leu	Ala	Val	Ala	Gln	Asn	Thr	Tyr	Ala	Val	Ser	
		75				80						85				90	
	tgg	ttt	aaa	ggc	aaa	gaa	tta	aac	ctg	gtg	ttt	gga	ctt	caa	ctt	agc	579
	Trp	Phe	Lys	Gly	Lys	Glu	Leu	Asn	Leu	Val	Phe	Gly	Leu	Gln	Leu	Ser	
20			95			100						105					
	atg	gct	aga	att	gga	agt	aca	gta	aac	atg	aac	ctc	atg	gga	tgg	ctg	627
	Met	Ala	Arg	Ile	Gly	Ser	Thr	Val	Asn	Met	Asn	Leu	Met	Gly	Trp	Leu	
			110			115						120					
	tat	tct	aag	att	gaa	gct	ttg	tta	ggg	tct	gct	ggg	cac	aca	acc	ctc	675
25	Tyr	Ser	Lys	Ile	Glu	Ala	Leu	Leu	Gly	Ser	Ala	Gly	His	Thr	Thr	Leu	

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	125	130	135	
	ggg atc aca ctt atg att ggg ggt ata acg tgt att ctt tca cta atc	723		
	Gly Ile Thr Leu Met Ile Gly Gly Ile Thr Cys Ile Leu Ser Leu Ile			
	140	145	150	
5	tgt gcc ttg gct ctt gcc tac ttg gat cag aga gca gag aga atc ctt	771		
	Cys Ala Leu Ala Leu Ala Tyr Leu Asp Gln Arg Ala Glu Arg Ile Leu			
	155	160	165	170
	cat aaa gaa caa gga aaa aca ggt gaa gtt att aaa tta act gat gta	819		
	His Lys Glu Gln Gly Lys Thr Gly Glu Val Ile Lys Leu Thr Asp Val			
10	175	180	185	
	aag gac ttc tcc tta ccc ctg tgg ctt ata ttt atc atc tgt gtc tgc	867		
	Lys Asp Phe Ser Leu Pro Leu Trp Leu Ile Phe Ile Ile Cys Val Cys			
	190	195	200	
	tat tat gtt gct gtg ttc cct ttt att gga ctt ggg aaa gtt ttc ttt	915		
15	Tyr Tyr Val Ala Val Phe Pro Phe Ile Gly Leu Gly Lys Val Phe Phe			
	205	210	215	
	aca gag aaa ttt gga ttt tct tcc cag gca gca agt gca att aac agt	963		
	Thr Glu Lys Phe Gly Phe Ser Ser Gln Ala Ala Ser Ala Ile Asn Ser			
	220	225	230	
20	gtt gta tat gtc ata tca gct ccc atg tcc ccg gtg ttt ggg ctc ctg	1011		
	Val Val Tyr Val Ile Ser Ala Pro Met Ser Pro Val Phe Gly Leu Leu			
	235	240	245	250
	gtg gat aaa aca ggg aag aac atc atc tgg gtt ctt tgc gca gta gca	1059		
	Val Asp Lys Thr Gly Lys Asn Ile Ile Trp Val Leu Cys Ala Val Ala			
25	255	260	265	

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 Ala Thr Leu Val Ser His Met Met Leu Ala Phe Thr Met Trp Asn Pro
 270 275 280
 tgg att gct atg tgt ctt ctg gga ctc tcc tac tca ttg ctt gcc tgt 1155
 5 Trp Ile Ala Met Cys Leu Leu Gly Leu Ser Tyr Ser Leu Leu Ala Cys
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 gca ttg tgg cca atg gtg gca ttt gta gtt cct gaa cat cag ctg gga 1203
 Ala Leu Trp Pro Met Val Ala Phe Val Val Pro Glu His Gln Leu Gly
 300 305 310
 10 act gca tat ggc ttc atg cag tcc att cag aat ctt ggg ttg gcc atc 1251
 Thr Ala Tyr Gly Phe Met Gln Ser Ile Gln Asn Leu Gly Leu Ala Ile
 315 320 325 330
 att tcc atc att gct ggt atg ata ctg gat tct cgg ggg tat ttg ttt 1299
 Ile Ser Ile Ile Ala Gly Met Ile Leu Asp Ser Arg Gly Tyr Leu Phe
 15 335 340 345
 ttg gaa gtg ttc ttc att gcc tgt gtt tct ttg tca ctt tta tct gtg 1347
 Leu Glu Val Phe Phe Ile Ala Cys Val Ser Leu Ser Leu Leu Ser Val
 350 355 360
 gtc tta ctc tat ttg gtg aat cgt gcc cag ggt ggg aac cta aat tat 1395
 20 Val Leu Leu Tyr Leu Val Asn Arg Ala Gln Gly Gly Asn Leu Asn Tyr
 365 370 375
 tct gca aga caa agg gaa gaa ata aaa ttt tcc cat act gaa tga 1440
 Ser Ala Arg Gln Arg Glu Glu Ile Lys Phe Ser His Thr Glu
 380 385 390
 25 gaagttaaaa tgaatgtgtc atgagaatgg gcttaacaca tcgttggttt gaaaacttcc 1500

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15 <211> 1934

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<213> Homo sapiens

<220>

20 <221> CDS

<222> (31)..(1647)

<400> 88

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Met Gly Cys Leu Trp Gly Leu Ala

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	Leu Pro Leu Phe Phe Phe Cys Trp Glu Val Gly Val Ser Gly Ser Ser				
	10 15 20				
5	gca ggc ccc agc acc cgc aga gca gac act gcg atg aca acg gac gac	150			
	Ala Gly Pro Ser Thr Arg Arg Ala Asp Thr Ala Met Thr Thr Asp Asp				
	25 30 35 40				
	aca gaa gtg ccc gct atg act cta gca ccg ggc cac gcc gct ctg gaa	198			
	Thr Glu Val Pro Ala Met Thr Leu Ala Pro Gly His Ala Ala Leu Glu				
10	45 50 55				
	act caa acg ctg agc gct gag acc tct tct agg gcc tca acc cca gcc	246			
	Thr Gln Thr Leu Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro Ala				
	60 65 70				
	ggc ccc att cca gaa gca gag acc agg gga gcc aag aga att tcc cct	294			
15	Gly Pro Ile Pro Glu Ala Glu Thr Arg Gly Ala Lys Arg Ile Ser Pro				
	75 80 85				
	gca aga gag acc agg agt ttc aca aaa aca tct ccc aac ttc atg gtg	342			
	Ala Arg Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met Val				
	90 95 100				
20	ctg atc gcc acc tcc gtg gag aca tca gcc gcc agt ggc agc ccc gag	390			
	Leu Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro Glu				
	105 110 115 120				
	gga gct gga atg acc aca gtt cag acc atc aca ggc agt gat ccc gag	438			
	Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro Glu				
25	125 130 135				

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	gaa gcc atc ttt gac acc ctt tgc acc gat gac agc tct gaa gag gca	486
	Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu Glu Ala	
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	aag aca ctc aca atg gac ata ttg aca ttg gct cac acc tcc aca gaa	534
5	Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr Ser Thr Glu	
	155 160 165	
	gct aag ggc ctg tcc tca gag agc agt gcc tct tcc gac ggc ccc cat	582
	Ala Lys Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His	
	170 175 180	
10	cca gtc atc acc ccg tca cgg gcc tca gag agc agc gcc tct tcc gac	630
	Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser Ser Ala Ser Ser Asp	
	185 190 195 200	
	ggc ccc cat cca gtc atc acc ccg tca cgg gcc tca gag agc agc gcc	678
	Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser Ser Ala	
15	205 210 215	
	tct tcc gac ggc ccc cat cca gtc atc acc ccc tca tgg tcc ccg gga	726
	Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Trp Ser Pro Gly	
	220 225 230	
	tct gat gtc act ctc ctc gct gaa gcc ctg gtg act gtc aca aac atc	774
20	Ser Asp Val Thr Leu Leu Ala Glu Ala Leu Val Thr Val Thr Asn Ile	
	235 240 245	
	gag gtt att aat tgc agc atc aca gaa ata gaa aca aca act tcc agc	822
	Glu Val Ile Asn Cys Ser Ile Thr Glu Ile Glu Thr Thr Thr Ser Ser	
	250 255 260	
25	atc cct ggg gcc tca gac ata gat ctc atc ccc acg gaa ggg gtg aag	870

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Ile Pro Gly Ala Ser Asp Ile Asp Leu Ile Pro Thr Glu Gly Val Lys
 265 270 275 280
 gcc tcg tcc acc tcc gat cca cca gct ctg cct gac tcc act gaa gca 918
 Ala Ser Ser Thr Ser Asp Pro Pro Ala Leu Pro Asp Ser Thr Glu Ala
 5 285 290 295
 aaa cca cac atc act gag gtc aca gcc tct gcc gag acc ctg tcc aca 966
 Lys Pro His Ile Thr Glu Val Thr Ala Ser Ala Glu Thr Leu Ser Thr
 300 305 310
 gcc ggc acc aca gag tca gct gca cct cat gcc acg gtt ggg acc cca 1014
 10 Ala Gly Thr Thr Glu Ser Ala Ala Pro His Ala Thr Val Gly Thr Pro
 315 320 325
 ctc ccc act aac agc gcc aca gaa aga gaa gtg aca gca ccc ggg gcc 1062
 Leu Pro Thr Asn Ser Ala Thr Glu Arg Glu Val Thr Ala Pro Gly Ala
 330 335 340
 15 acg acc ctc agt gga gct ctg gtc aca gtt agc agg aat ccc ctg gaa 1110
 Thr Thr Leu Ser Gly Ala Leu Val Thr Val Ser Arg Asn Pro Leu Glu
 345 350 355 360
 gaa acc tca gcc ctc tct gtt gag aca cca agt tac gtc aaa gtc tca 1158
 Glu Thr Ser Ala Leu Ser Val Glu Thr Pro Ser Tyr Val Lys Val Ser
 20 365 370 375
 gga gca gct ccg gtc tcc ata gag gct ggg tca gca gtg ggc aaa aca 1206
 Gly Ala Ala Pro Val Ser Ile Glu Ala Gly Ser Ala Val Gly Lys Thr
 380 385 390
 act tcc ttt gct ggg agc tct gct tcc tcc tac agc ccc tcg gaa gcc 1254
 25 Thr Ser Phe Ala Gly Ser Ser Ala Ser Ser Tyr Ser Pro Ser Glu Ala

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	395	400	405	
	gcc ctc aag aac ttc acc cct tca gag aca ccg acc atg gac atc gca			1302
	Ala Leu Lys Asn Phe Thr Pro Ser Glu Thr Pro Thr Met Asp Ile Ala			
	410	415	420	
5	acc aag ggg ccc ttc ccc acc agc agg gac cct ctt cct tct gtc cct			1350
	Thr Lys Gly Pro Phe Pro Thr Ser Arg Asp Pro Leu Pro Ser Val Pro			
	425	430	435	440
	ccg act aca acc aac agc agc cga ggg acg aac agc acc tta gcc aag			1398
	Pro Thr Thr Thr Asn Ser Ser Arg Gly Thr Asn Ser Thr Leu Ala Lys			
10	445	450	455	
	atc aca acc tca gcg aag acc acg atg aag ccc cca aca gcc acg ccc			1446
	Ile Thr Thr Ser Ala Lys Thr Thr Met Lys Pro Pro Thr Ala Thr Pro			
	460	465	470	
	acg act gcc cgg acg agg ccg acc aca gac gtg agt gca ggt gaa aat			1494
15	Thr Thr Ala Arg Thr Arg Pro Thr Thr Asp Val Ser Ala Gly Glu Asn			
	475	480	485	
	gga ggt ttc ctc ctc ctg cgg ctg agt gtg gct tcc ccg gaa gac ctc			1542
	Gly Gly Phe Leu Leu Leu Arg Leu Ser Val Ala Ser Pro Glu Asp Leu			
	490	495	500	
20	act gac ccc aga gtg gca gaa agg ctg atg cag cag ctc cac cgg gaa			1590
	Thr Asp Pro Arg Val Ala Glu Arg Leu Met Gln Gln Leu His Arg Glu			
	505	510	515	520
	ctc cac gcc cac gcg cct cac ttc cag gtc tcc tta ctg cgt gtc agg			1638
	Leu His Ala His Ala Pro His Phe Gln Val Ser Leu Leu Arg Val Arg			
25	525	530	535	

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aga ggc taa cggacatcag ctgcagccag gcatgtcccg tatgccaaaa 1687

Arg Gly

gaggggtgctg cccctagcct gggccccac cgacagactg cagctgcgtt actgtgctga 1747

gaggtaccca gaaggttccc atgacgggca gcatgtccaa gcccctaacc ccagatgtgg 1807

5 caacaggacc ctcgctcaca tccaccggag tgtatgtatg gggaggggct tcacctgttc 1867

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atcacccc 1934

<210> 89

10 <211> 1880

<212> DNA

<213> Homo sapiens

<220>

15 <221> CDS

<222> (71)..(379)

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Met Glu Ala Ala Leu Leu Gly Leu Cys Asn Trp Ser Thr

1

5

10

ctg ggc gtg tgc gcc gcg ctg aag ctg ccg cag atc tcc gct gtg cta 157

Leu Gly Val Cys Ala Ala Leu Lys Leu Pro Gln Ile Ser Ala Val Leu

25

15

20

25

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gcg gcg cgc agc gcg cgg ggc ctc agc ctt ccg agt tta ctt ctg gag 205
 Ala Ala Arg Ser Ala Arg Gly Leu Ser Leu Pro Ser Leu Leu Leu Glu
 30 35 40 45
 ctg gca gga ttc ctg gtg ttt ctg cgg tac cag tgt tac tat ggg tat 253
 5 Leu Ala Gly Phe Leu Val Phe Leu Arg Tyr Gln Cys Tyr Tyr Gly Tyr
 50 55 60
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 Pro Pro Leu Thr Tyr Leu Glu Tyr Pro Ile Leu Ile Ala Gln Asp Val
 65 70 75
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 Ile Leu Leu Leu Cys Ile Phe His Phe Asn Gly Asn Val Lys Gln Ala
 80 85 90
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 25 agtaaatacag tttataatct ttaaagccaa aggttttttt agacttgaaa gaaagagcca 999

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gttgagatta ttatatactg tattttcttc taaattaacc ctaatgttta aaaactcact 1779
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<211> 2295

<212> DNA

20 <213> Homo sapiens

<220>

<221> CDS

<222> (55)..(1383)

25

213/346

<400> 90

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   Gly Leu Ala Met Glu His Gly Gly Ser Tyr Ala Arg Ala Gly Gly Ser
           5              10              15
tct cgg ggc tgc tgg tat tac ctg cgc tac ttc ttc ctc ttc gtc tcc 153
   Ser Arg Gly Cys Trp Tyr Tyr Leu Arg Tyr Phe Phe Leu Phe Val Ser
10           20              25              30
ctc atc caa ttc ctc atc atc ctg ggg ctc gtg ctc ttc atg gtc tat 201
   Leu Ile Gln Phe Leu Ile Ile Leu Gly Leu Val Leu Phe Met Val Tyr
           35              40              45
ggc aac gtg cac gtg agc aca gag tcc aac ctg cag gcc acc gag cgc 249
15  Gly Asn Val His Val Ser Thr Glu Ser Asn Leu Gln Ala Thr Glu Arg
           50              55              60              65
cga gcc gag ggc cta tac agt cag ctc cta ggg ctc acg gcc tcc cag 297
   Arg Ala Glu Gly Leu Tyr Ser Gln Leu Leu Gly Leu Thr Ala Ser Gln
           70              75              80
20  tcc aac ttg acc aag gag ctc aac ttc acc acc cgc gcc aag gat gcc 345
   Ser Asn Leu Thr Lys Glu Leu Asn Phe Thr Thr Arg Ala Lys Asp Ala
           85              90              95
atc atg cag atg tgg ctg aat gct cgc cgc gac ctg gac cgc atc aat 393
   Ile Met Gln Met Trp Leu Asn Ala Arg Arg Asp Leu Asp Arg Ile Asn
25           100              105              110

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 Ala Ser Phe Arg Gln Cys Gln Gly Asp Arg Val Ile Tyr Thr Asn Asn
 115 120 125
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 5 Gln Arg Tyr Met Ala Ala Ile Ile Leu Ser Glu Lys Gln Cys Arg Asp
 130 135 140 145
 caa ttc aag gac atg aac aag agc tgc gat gcc ttg ctc ttc atg ctg 537
 Gln Phe Lys Asp Met Asn Lys Ser Cys Asp Ala Leu Leu Phe Met Leu
 150 155 160
 10 aat cag aag gtg aag acg ctg gag gtg gag ata gcc aag gag aag acc 585
 Asn Gln Lys Val Lys Thr Leu Glu Val Glu Ile Ala Lys Glu Lys Thr
 165 170 175
 att tgc act aag gat aag gaa agc gtg ctg ctg aac aaa cgc gtg gcg 633
 Ile Cys Thr Lys Asp Lys Glu Ser Val Leu Leu Asn Lys Arg Val Ala
 15 180 185 190
 gag gaa cag ctg gtt gaa tgc gtg aaa acc cgg gag ctg cag cac caa 681
 Glu Glu Gln Leu Val Glu Cys Val Lys Thr Arg Glu Leu Gln His Gln
 195 200 205
 gag cgc cag ctg gcc aag gag caa ctg caa aag gtg caa gcc ctc tgc 729
 20 Glu Arg Gln Leu Ala Lys Glu Gln Leu Gln Lys Val Gln Ala Leu Cys
 210 215 220 225
 ctg ccc ctg gac aag gac aag ttt gag atg gac ctt cgt aac ctg tgg 777
 Leu Pro Leu Asp Lys Asp Lys Phe Glu Met Asp Leu Arg Asn Leu Trp
 230 235 240
 25 agg gac tcc att atc cca cgc agc ctg gac aac ctg ggt tac aac ctc 825

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	Arg Asp Ser Ile Ile Pro Arg Ser Leu Asp Asn Leu Gly Tyr Asn Leu	
	245	250 255
	tac cat ccc ctg ggc tgc gaa ttg gcc tcc atc cgc aga gcc tgc gac	873
	Tyr His Pro Leu Gly Ser Glu Leu Ala Ser Ile Arg Arg Ala Cys Asp	
5	260	265 270
	cac atg ccc agc ctc atg agc tcc aag gtg gag gag ctg gcc cgg agc	921
	His Met Pro Ser Leu Met Ser Ser Lys Val Glu Glu Leu Ala Arg Ser	
	275	280 285
	ctc cgg gcg gat atc gaa cgc gtg gcc cgc gag aac tca gac ctc caa	969
10	Leu Arg Ala Asp Ile Glu Arg Val Ala Arg Glu Asn Ser Asp Leu Gln	
	290	295 300 305
	cgc cag aag ctg gaa gcc cag cag ggc ctg cgg gcc agt cag gag gcg	1017
	Arg Gln Lys Leu Glu Ala Gln Gln Gly Leu Arg Ala Ser Gln Glu Ala	
	310	315 320
15	aaa cag aag gtg gag aag gag gct cag gcc cgg gag gcc aag ctc caa	1065
	Lys Gln Lys Val Glu Lys Glu Ala Gln Ala Arg Glu Ala Lys Leu Gln	
	325	330 335
	gct gaa tgc tcc cgg cag acc cag cta gcg ctg gag gag aag gcg gtg	1113
	Ala Glu Cys Ser Arg Gln Thr Gln Leu Ala Leu Glu Glu Lys Ala Val	
20	340	345 350
	ctg cgg aag gaa cga gac aac ctg gcc aag gag ctg gaa gag aag aag	1161
	Leu Arg Lys Glu Arg Asp Asn Leu Ala Lys Glu Leu Glu Glu Lys Lys	
	355	360 365
	agg gag gcg gag cag ctc agg atg gag ctg gcc atc aga aac tca gcc	1209
25	Arg Glu Ala Glu Gln Leu Arg Met Glu Leu Ala Ile Arg Asn Ser Ala	

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370 375 380 385
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 390 395 400
 5 agg ccc atg ggc cct gtc ccc aac ccc cag ccc atc gac cca gct agc 1305
 Arg Pro Met Gly Pro Val Pro Asn Pro Gln Pro Ile Asp Pro Ala Ser
 405 410 415
 ctg gag gag ttc aag agg aag atc ctg gag tcc cag agg ccc cct gca 1353
 Leu Glu Glu Phe Lys Arg Lys Ile Leu Glu Ser Gln Arg Pro Pro Ala
 10 420 425 430
 ggc atc cct gta gcc cca tcc agt ggc tga ggaggctcca ggcctgagga 1403
 Gly Ile Pro Val Ala Pro Ser Ser Gly
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<212> PRT

<213> Homo sapiens

10 <400> 91

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20 25 30

15 His Ile Gly Glu Thr Glu Lys Arg Cys Phe Ile Glu Glu Ile Pro Asp

35 40 45

Glu Thr Met Val Ile Gly Asn Tyr Arg Thr Gln Met Trp Asp Lys Gln

50 55 60

Lys Glu Val Phe Leu Pro Ser Thr Pro Gly Leu Gly Met His Val Glu

20 65 70 75 80

Val Lys Asp Pro Asp Gly Lys Val Val Leu Ser Arg Gln Tyr Gly Ser

85 90 95

Glu Gly Arg Phe Thr Phe Thr Ser His Thr Pro Gly Asp His Gln Ile

100 105 110

25 Cys Leu His Ser Asn Ser Thr Arg Met Ala Leu Phe Ala Gly Gly Lys

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115 120 125
Leu Arg Val His Leu Asp Ile Gln Val Gly Glu His Ala Asn Asn Tyr
130 135 140
Pro Glu Ile Ala Ala Lys Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala
5 145 150 155 160
Arg Gln Leu Leu Asp Gln Val Glu Gln Ile Gln Lys Glu Gln Asp Tyr
165 170 175
Gln Arg Tyr Arg Glu Glu Arg Phe Arg Leu Thr Ser Glu Ser Thr Asn
180 185 190
10 Gln Arg Val Leu Trp Trp Ser Ile Ala Gln Thr Val Ile Leu Ile Leu
195 200 205
Thr Gly Ile Trp Gln Met Arg His Leu Lys Ser Phe Phe Glu Ala Lys
210 215 220
Lys Leu Val
15 225

<210> 92
<211> 352
<212> PRT
20 <213> Homo sapiens

<400> 92
Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly
1 5 10 15
25 Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys

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	20	25	30
	Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly		
	35	40	45
	Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro		
5	50	55	60
	Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn		
	65	70	75
	Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu		
	85	90	95
10	Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp		
	100	105	110
	Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu		
	115	120	125
	Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro		
15	130	135	140
	Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His		
	145	150	155
	Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly		
	165	170	175
20	Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly		
	180	185	190
	Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val		
	195	200	205
	Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln		
25	210	215	220

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Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
225 230 235 240
Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe
245 250 255
5 Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
260 265 270
Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
275 280 285
Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val
10 290 295 300
Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
305 310 315 320
Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
325 330 335
15 Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser
340 345 350

<210> 93

20 <211> 130

<212> PRT

<213> Homo sapiens

<400> 93

25 Met Ser Ser Ser Gly Gly Ala Pro Gly Ala Ser Ala Ser Ser Ala Pro

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1 5 10 15
Pro Ala Gln Glu Glu Gly Met Thr Trp Trp Tyr Arg Trp Leu Cys Arg
20 25 30
Leu Ser Gly Val Leu Gly Ala Val Ser Cys Ala Ile Ser Gly Leu Phe
5 35 40 45
Asn Cys Ile Thr Ile His Pro Leu Asn Ile Ala Ala Gly Val Trp Met
50 55 60
Met Met Ala Val Val Pro Ile Val Ile Ser Leu Thr Leu Thr Thr Leu
65 70 75 80
10 Leu Gly Asn Ala Ile Ala Phe Ala Thr Gly Val Leu Tyr Gly Leu Ser
85 90 95
Ala Leu Gly Lys Lys Gly Asp Ala Ile Ser Tyr Ala Arg Ile Gln Gln
100 105 110
Gln Arg Gln Gln Ala Asp Glu Glu Lys Leu Ala Glu Thr Leu Glu Gly
15 115 120 125
Glu Leu
130

<210> 94

20 <211> 330

<212> PRT

<213> Homo sapiens

<400> 94

25 Met Ser Arg Cys Ala Gln Ala Ala Glu Val Ala Ala Thr Val Pro Gly

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	1	5	10	15
	Ala Gly Val Gly Asn Val Gly Leu Arg Pro Pro Met Val Pro Arg Gln			
	20	25	30	
	Ala Ser Phe Phe Pro Pro Pro Val Pro Asn Pro Phe Val Gln Gln Thr			
5	35	40	45	
	Gln Ile Gly Ser Ala Arg Arg Val Gln Ile Val Leu Leu Gly Ile Ile			
	50	55	60	
	Leu Leu Pro Ile Arg Val Leu Leu Val Ala Leu Ile Leu Leu Leu Ala			
	65	70	75	80
10	Trp Pro Phe Ala Ala Ile Ser Thr Val Cys Cys Pro Glu Lys Leu Thr			
	85	90	95	
	His Pro Ile Thr Gly Trp Arg Arg Lys Ile Thr Gln Thr Ala Leu Lys			
	100	105	110	
	Phe Leu Gly Arg Ala Met Phe Phe Ser Met Gly Phe Ile Val Ala Val			
15	115	120	125	
	Lys Gly Lys Ile Ala Ser Pro Leu Glu Ala Pro Val Phe Val Ala Ala			
	130	135	140	
	Pro His Ser Thr Phe Phe Asp Gly Ile Ala Cys Val Val Ala Gly Leu			
	145	150	155	160
20	Pro Ser Ile Val Ser Arg Asn Glu Asn Ala Gln Val Pro Leu Ile Gly			
	165	170	175	
	Arg Leu Leu Arg Ala Val Gln Pro Val Leu Val Ser Arg Val Asp Pro			
	180	185	190	
	Asp Ser Arg Lys Asn Thr Ile Asn Glu Ile Ile Lys Arg Thr Thr Ser			
25	195	200	205	

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Gly Gly Glu Trp Pro Gln Ile Leu Val Phe Pro Glu Gly Thr Cys Thr
 210 215 220
 Asn Arg Ser Cys Leu Ile Thr Phe Lys Pro Gly Ala Phe Ile Pro Gly
 225 230 235 240
 5 Val Pro Val Gln Pro Val Leu Leu Arg Tyr Pro Asn Lys Leu Asp Thr
 245 250 255
 Val Thr Trp Thr Trp Gln Gly Tyr Thr Phe Ile Gln Leu Cys Met Leu
 260 265 270
 Thr Phe Cys Gln Leu Phe Thr Lys Val Glu Val Glu Met Phe Leu Phe
 10 275 280 285
 Phe Trp Glu Gly Ser Ser Lys His Cys Leu Lys Ile Ser Ser Phe Phe
 290 295 300
 Cys Ile Phe Ser Leu Arg Arg Phe Lys Arg Arg Ile Thr Gln Arg Thr
 305 310 315 320
 15 Arg Thr Ala His Leu Leu Arg Leu Ser Phe
 325 330

 <210> 95
 <211> 350
 20 <212> PRT
 <213> Homo sapiens

 <400> 95
 Met Ala Leu Pro Pro Gly Pro Ala Ala Leu Arg His Thr Leu Leu Leu
 25 1 5 10 15

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Leu Pro Ala Leu Leu Ser Ser Gly Gly Pro Gly Thr Pro Arg Leu Ala
20 25 30

Trp Tyr Leu Asp Gly Gln Leu Gln Glu Ala Ser Thr Ser Arg Leu Leu
35 40 45

5 Ser Val Gly Gly Glu Ala Phe Ser Gly Gly Thr Ser Thr Phe Thr Val
50 55 60

Thr Ala His Arg Ala Gln His Glu Leu Asn Cys Ser Leu Gln Asp Pro
65 70 75 80

Arg Ser Gly Arg Ser Ala Asn Ala Ser Val Ile Leu Asn Val Gln Phe
10 85 90 95

Lys Pro Glu Ile Ala Gln Val Gly Ala Lys Tyr Gln Glu Ala Gln Gly
100 105 110

Pro Gly Leu Leu Val Val Leu Phe Ala Leu Val Arg Ala Asn Pro Pro
115 120 125

15 Ala Asn Val Thr Trp Ile Asp Gln Asp Gly Pro Val Thr Val Asn Thr
130 135 140

Ser Asp Phe Leu Val Leu Asp Ala Gln Asn Tyr Pro Trp Leu Thr Asn
145 150 155 160

His Thr Val Gln Leu Gln Leu Arg Ser Leu Ala His Asn Leu Ser Val
20 165 170 175

Val Ala Thr Asn Asp Val Gly Val Thr Ser Ala Ser Leu Pro Ala Pro
180 185 190

Gly Leu Leu Ala Thr Arg Val Glu Val Pro Leu Leu Gly Ile Val Val
195 200 205

25 Ala Ala Gly Leu Ala Leu Gly Thr Leu Val Gly Phe Ser Thr Leu Val

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210 215 220
Ala Cys Leu Val Cys Arg Lys Glu Lys Lys Thr Lys Gly Pro Ser Arg
225 230 235 240
His Pro Ser Leu Ile Ser Ser Asp Ser Asn Asn Leu Lys Leu Asn Asn
5 245 250 255
Val Arg Leu Pro Arg Glu Asn Met Ser Leu Pro Ser Asn Leu Gln Leu
260 265 270
Asn Asp Leu Thr Pro Asp Ser Arg Ala Val Lys Pro Ala Asp Arg Gln
275 280 285
10 Met Ala Gln Asn Asn Ser Arg Pro Glu Leu Leu Asp Pro Glu Pro Gly
290 295 300
Gly Leu Leu Thr Ser Gln Ala Cys Leu Leu His His Gly Thr Pro Ala
305 310 315 320
Leu Thr Asn Pro Trp Leu Pro His Gln Gln Glu Gly Ala Leu Pro Gly
15 325 330 335
Gly Trp Ser Pro Gln Ala His Asn Ser Thr Val Trp Lys Leu
340 345 350

<210> 96
20 <211> 113
<212> PRT
<213> Homo sapiens

<400> 96
25 Met Asn Glu Thr Asn Lys Thr Leu Val Gly Pro Ser Glu Leu Pro Thr

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1 5 10 15
 Ala Ser Ala Val Ala Pro Gly Pro Gly Thr Gly Ala Arg Ala Trp Pro
 20 25 30
 Val Leu Val Gly Phe Val Leu Gly Ala Val Val Leu Ser Leu Leu Ile
 5 35 40 45
 Ala Leu Ala Ala Lys Cys His Leu Cys Arg Arg Tyr His Ala Ser Tyr
 50 55 60
 Arg His Arg Pro Leu Pro Glu Thr Gly Arg Gly Gly Arg Pro Gln Val
 65 70 75 80
 10 Ala Glu Asp Glu Asp Asp Asp Gly Phe Ile Glu Asp Asn Tyr Ile Gln
 85 90 95
 Pro Gly Thr Gly Glu Leu Gly Thr Glu Gly Ser Arg Asp His Phe Ser
 100 105 110
 Leu
 15

<210> 97

<211> 189

<212> PRT

20 <213> Homo sapiens

<400> 97

Met Ala Leu Leu Ser Arg Pro Ala Leu Thr Leu Leu Leu Leu Met
 1 5 10 15
 25 Ala Ala Val Val Arg Cys Gln Glu Gln Ala Gln Thr Thr Asp Trp Arg

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20 25 30
Ala Thr Leu Lys Thr Ile Arg Asn Gly Val His Lys Ile Asp Thr Tyr
35 40 45
Leu Asn Ala Ala Leu Asp Leu Leu Gly Gly Glu Asp Gly Leu Cys Gln
5 50 55 60
Tyr Lys Cys Ser Asp Gly Ser Lys Pro Phe Pro Arg Tyr Gly Tyr Lys
65 70 75 80
Pro Ser Pro Pro Asn Gly Cys Gly Ser Pro Leu Phe Gly Val His Leu
85 90 95
10 Asn Ile Gly Ile Pro Ser Leu Thr Lys Cys Cys Asn Gln His Asp Arg
100 105 110
Cys Tyr Glu Thr Cys Gly Lys Ser Lys Asn Asp Cys Asp Glu Glu Phe
115 120 125
Gln Tyr Cys Leu Ser Lys Ile Cys Arg Asp Val Gln Lys Thr Leu Gly
15 130 135 140
Leu Thr Gln His Val Gln Ala Cys Glu Thr Thr Val Glu Leu Leu Phe
145 150 155 160
Asp Ser Val Ile His Leu Gly Cys Lys Pro Tyr Leu Asp Ser Gln Arg
165 170 175
20 Ala Ala Cys Arg Cys His Tyr Glu Glu Lys Thr Asp Leu
180 185

<210> 98

<211> 277

25 <212> PRT

228/346

<213> Homo sapiens

<400> 98

Met Ser Pro Leu Leu Gly Leu Arg Ser Glu Leu Gln Asp Thr Cys Thr
5 1 5 10 15
Ser Leu Gly Leu Met Leu Ser Val Val Leu Leu Met Gly Leu Ala Arg
 20 25 30
Val Val Ala Arg Gln Gln Leu His Arg Pro Val Ala His Ala Phe Val
 35 40 45
10 Leu Glu Phe Leu Ala Thr Phe Gln Leu Cys Cys Cys Thr His Glu Leu
 50 55 60
Gln Leu Leu Ser Glu Gln His Pro Ala His Pro Thr Trp Thr Leu Thr
 65 70 75 80
Leu Val Tyr Phe Phe Ser Leu Val His Gly Leu Thr Leu Val Gly Thr
15 85 90 95
Ser Ser Asn Pro Cys Gly Val Met Met Gln Met Met Leu Gly Gly Met
 100 105 110
Ser Pro Glu Thr Gly Ala Val Arg Leu Leu Ala Gln Leu Val Ser Ala
 115 120 125
20 Leu Cys Ser Arg Tyr Cys Thr Ser Ala Leu Trp Ser Leu Gly Leu Thr
 130 135 140
Gln Tyr His Val Ser Glu Arg Ser Phe Ala Cys Lys Asn Pro Ile Arg
 145 150 155 160
Val Asp Leu Leu Lys Ala Val Ile Thr Glu Ala Val Cys Ser Phe Leu
25 165 170 175

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Phe His Ser Ala Leu Leu His Phe Gln Glu Val Arg Thr Lys Leu Arg
180 185 190

Ile His Leu Leu Ala Ala Leu Ile Thr Phe Leu Val Tyr Ala Gly Gly
195 200 205

5 Ser Leu Thr Gly Ala Val Phe Asn Pro Ala Leu Ala Leu Ser Leu His
210 215 220

Phe Met Cys Phe Asp Glu Ala Phe Pro Gln Phe Phe Ile Val Tyr Trp
225 230 235 240

Leu Ala Pro Ser Leu Gly Ile Leu Leu Met Ile Leu Met Phe Ser Phe
10 245 250 255

Phe His Gly Cys Ile Thr Thr Ile Gln Leu Ile Lys Arg Asn Asn Cys
260 265 270

Ser Lys Asp Ser Asp
275

15

<210> 99

<211> 274

<212> PRT

<213> Homo sapiens

20

<400> 99

Met Gly Lys Ser Leu Ser His Leu Pro Leu His Ser Ser Lys Glu Asp
1 5 10 15

Ala Tyr Asp Gly Val Thr Ser Glu Asn Met Arg Asn Gly Leu Val Asn
25 20 25 30

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Ser Glu Val His Asn Glu Asp Gly Arg Asn Gly Asp Val Ser Gln Phe
 35 40 45
 Pro Tyr Val Glu Phe Thr Gly Arg Asp Ser Val Thr Cys Pro Thr Cys
 50 55 60
 5 Gln Gly Thr Gly Arg Ile Pro Arg Gly Gln Glu Asn Gln Leu Val Ala
 65 70 75 80
 Leu Ile Pro Tyr Ser Asp Gln Arg Leu Arg Pro Arg Arg Thr Lys Leu
 85 90 95
 Tyr Val Met Ala Ser Val Phe Val Cys Leu Leu Leu Ser Gly Leu Ala
 10 100 105 110
 Val Phe Phe Leu Phe Pro Arg Ser Ile Asp Val Lys Tyr Ile Gly Val
 115 120 125
 Lys Ser Ala Tyr Val Ser Tyr Asp Val Gln Lys Arg Thr Ile Tyr Leu
 130 135 140
 15 Asn Ile Thr Asn Thr Leu Asn Ile Thr Asn Asn Asn Tyr Tyr Ser Val
 145 150 155 160
 Glu Val Glu Asn Ile Thr Ala Gln Val Gln Phe Ser Lys Thr Val Ile
 165 170 175
 Gly Lys Ala Arg Leu Asn Asn Ile Thr Ile Ile Gly Pro Leu Asp Met
 20 180 185 190
 Lys Gln Ile Asp Tyr Thr Val Pro Thr Val Ile Ala Glu Glu Met Ser
 195 200 205
 Tyr Met Tyr Asp Phe Cys Thr Leu Ile Ser Ile Lys Val His Asn Ile
 210 215 220
 25 Val Leu Met Met Gln Val Thr Val Thr Thr Thr Tyr Phe Gly His Ser

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225 230 235 240
Glu Gln Ile Ser Gln Glu Arg Tyr Gln Tyr Val Asp Cys Gly Arg Asn
245 250 255
Thr Thr Tyr Gln Leu Gly Gln Ser Glu Tyr Leu Asn Val Leu Gln Pro
5 260 265 270
Gln Gln

<210> 100
10 <211> 390
<212> PRT
<213> Homo sapiens

<400> 100
15 Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu
1 5 10 15
Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln
20 25 30
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val
20 35 40 45
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln
50 55 60
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys
65 70 75 80
25 Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro

		85		90		95										
	Gly	Val	Ser	Leu	Val	Tyr	Ser	Met	Pro	Ser	Arg	Asn	Leu	Ser	Leu	Arg
				100					105					110		
	Leu	Glu	Gly	Leu	Gln	Glu	Lys	Asp	Ser	Gly	Pro	Tyr	Ser	Cys	Ser	Val
5			115					120						125		
	Asn	Val	Gln	Asp	Lys	Gln	Gly	Lys	Ser	Arg	Gly	His	Ser	Ile	Lys	Thr
		130					135						140			
	Leu	Glu	Leu	Asn	Val	Leu	Val	Pro	Pro	Ala	Pro	Pro	Ser	Cys	Arg	Leu
	145					150					155				160	
10	Gln	Gly	Val	Pro	His	Val	Gly	Ala	Asn	Val	Thr	Leu	Ser	Cys	Gln	Ser
				165						170					175	
	Pro	Arg	Ser	Lys	Pro	Ala	Val	Gln	Tyr	Gln	Trp	Asp	Arg	Gln	Leu	Pro
			180						185					190		
	Ser	Phe	Gln	Thr	Phe	Phe	Ala	Pro	Ala	Leu	Asp	Val	Ile	Arg	Gly	Ser
15			195						200					205		
	Leu	Ser	Leu	Thr	Asn	Leu	Ser	Ser	Ser	Met	Ala	Gly	Val	Tyr	Val	Cys
		210					215					220				
	Lys	Ala	His	Asn	Glu	Val	Gly	Thr	Ala	Gln	Cys	Asn	Val	Thr	Leu	Glu
	225					230					235				240	
20	Val	Ser	Thr	Gly	Pro	Gly	Ala	Ala	Val	Val	Ala	Gly	Ala	Val	Val	Gly
				245						250					255	
	Thr	Leu	Val	Gly	Leu	Gly	Leu	Leu	Ala	Gly	Leu	Val	Leu	Leu	Tyr	His
			260						265					270		
	Cys	Arg	Gly	Lys	Ala	Leu	Glu	Glu	Pro	Ala	Asn	Asp	Ile	Lys	Glu	Asp
25			275						280					285		

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Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
 290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
 305 310 315 320

5 Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
 10 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
 370 375 380

Gln Ala Gly Ser Leu Val
 385 390

15

<210> 101

<211> 684

<212> DNA

<213> Homo sapiens

20

<400> 101

atggcaggtg tcggggctgg gcctctgcgg gcgatggggc ggcaggccct gctgcttctc 60

gogctgtgcg ccacaggcgc ccaggggctc tacttccaca tcggcgagac cgagaagcgc 120

tgtttcatcg aggaaatccc cgacgagacc atggtcacg gcaactatcg taccagatg 180

25 tgggataagc agaaggaggt cttcctgccc tcgaccctg gcctgggcat gcacgtggaa 240

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gtgaaggacc ccgacggcaa ggtggtgctg tcccggcagt acggctcgga gggccgcttc 300
acgttcacct cccacacgcc cggtgaccat caaatctgtc tgcactccaa ttctaccagg 360
atggctctct tcgctggtgg caaactgcgg gtgcatctcg acatccaggt tggggagcat 420
gccaacaact accctgagat tgctgcaaaa gataagctga cggagctaca gctccgcgcc 480
5 cgccagttgc ttgatcaggt ggaacagatt cagaaggagc aggattacca aaggtatcgt 540
gaagagcgct tccgactgac gagcgagagc accaaccaga gggtcctatg gtggtccatt 600
gctcagactg tcatcctcat cctcactggc atctggcaga tgcgtcacct caagagcttc 660
tttgaggcca agaagctggt gtag 684

10 <210> 102
<211> 1059
<212> DNA
<213> Homo sapiens

15 <400> 102
atggagagcg gagggcggcc ctcgctgtgc cagttcatcc tcctgggcac cacctctgtg 60
gtcaccgccg ccctgtactc cgtgtaccgg cagaaggccc gggctctcca agagctcaag 120
ggagctaaaa aagttcattt ggggtgaagat ttaaagagta ttctttcaga agctccagga 180
aaatgcgtgc cttatgctgt tatagaagga gctgtgcggt ctgttaaaga aacgcttaac 240
20 agccagtttg tggaaaactg caagggggta attcagcggc tgacacttca ggagcacaag 300
atggtgtgga atcgaaccac ccacctttgg aatgattgct caaagatcat tcacagagg 360
accaacacag tgccctttga cctggtgccc cagcaggatg gcgtggatgt ggctgtgcga 420
gtgctgaagc ccctggactc agtggatctg ggtctagaga ctgtgtatga gaagttccac 480
ccctcgattc agtccttcac cgatgtcatc ggccactaca tcagcgggtga gcggcccaaa 540
25 ggcatccaag agaccgagga gatgctgaag gtgggggcca ccctcacagg ggttggcgaa 600

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ctggtcctgg acaacaactc tgtccgcctg cagccgcca aacaaggcat gcagtactat 660
ctaagcagcc aggacttcga cagcctgctg cagaggcagg agtcgagcgt caggctctgg 720
aaggtgctgg cgctggtttt tggctttgcc acatgtgcca ccctcttctt cattctccgg 780
aagcagtatc tgcagcggca ggagcgctg cgcctcaagc agatgcagga ggagttccag 840
5 gagcatgagg ccagctgct gagccgagcc aagcctgagg acagggagag tctgaagagc 900
gcctgtgtag tgtgtctgag cagcttcaag tctgctgtct ttctggagtg tgggcacgtt 960
tgttcctgca ccgagtgcta ccgcgccttg ccagagccca agaagtgcc tatctgcaga 1020
caggcgatca cccgggtgat acccctgtac aacagctaa 1059

10 <210> 103
<211> 393
<212> DNA
<213> Homo sapiens

15 <400> 103
atgagcagct caggtggggc gcccggggcg tccgccagct ctgcgcgcgc cgcgcaggaa 60
gagggcatga cgtggtggta ccgctggctg tgtcgctgt ctggggtgct gggggcagtc 120
tcttgcgca tctctggcct cttcaactgc atcaccatcc accctctgaa catcgcgcc 180
ggcgtgtgga tgatgatggc ggtcgttccc atcgtcatca gcctgaccct gaccacgtg 240
20 ctgggcaacg ccatcgctt tgctacggg gtgctgtacg gactctctgc tctgggcaaa 300
aagggcgatg cgatctccta tgccaggatc cagcagcaga ggacgcaggc ggatgaggag 360
aagctcgcg agaccctgga gggggagctg tga 393

<210> 104
25 <211> 993

236/346

<212> DNA

<213> Homo sapiens

<400> 104

5 atgagccggt ggcgccaggc ggcggaagtg gcggccacag tgccagggtgc cggcgtcggg 60
aacgtggggc tgcggccgcc catggtgccc cgtcaggcgt ccttcttccc gccgccggtg 120
ccgaacccct tcgtgcagca gacgcagatc ggctccgca ggcgggtcca gattgtcctt 180
cttgggatta tcttgcttcc aattcgtgtc ttattgggtg cgtaatttt attacttgca 240
tggccatttg ctgcaatttc aacagtatgc tgcctgaaa agctgacca cccaataact 300
10 ggttgaggga ggaaaattac tcaaacagct ttgaaatttc tgggtcgtgc tatgttcttt 360
tcaatgggat ttatagttgc tgtaaagga aagattgcaa gtcctttgga agcaccagtt 420
tttgttgctg cccctcattc aacattcttt gatggaattg cctgtgttgt agctgggtta 480
ccttctatag tatctgaaa tgagaatgca cadgtccctc tgattggcag actgttacgg 540
gctgtgcaac cagttttggt gtcccggtga gatccggatt cccgaaaaa cacaataaat 600
15 gaaataataa agcgaacaac atcaggagga gaatggcccc agatactagt tttccagaa 660
ggtacttgta ctaatcgttc ctgtttgatt acttttaaac caggagcctt cattccagga 720
gttccagtgc agccagtcct cctcagatac ccaaacaagc tggatactgt gacctggaca 780
tggcaaggat atacattcat tcagctttgt atgcttactt tctgccagct cttcaciaag 840
gtagaagttg agatgtttct gttcttttgg gaaggaagca gcaagcattg tttaaaaata 900
20 tcttcttct tttgcatttt ttctcttoga agatttaaaa gaagaattac acaaagaact 960
agaactgcac atttggttaag attgtccttt taa 993

<210> 105

<211> 1053

25 <212> DNA

237/346

<213> Homo sapiens

<400> 105

atggcgctgc ctccaggccc agccgccctc cggcacacac tgctgctcct gccagccctt 60
5 ctgagctcag gtgggcctgg cacccccaga ttggcctggg atctggatgg acagctgcag 120
gaggccagca cctcaagact gctgagcgtg ggaggggagg ctttctctgg aggcaccagc 180
accttcaactg tcaactgccca tcggggcccag catgagctca actgctctct gcaggacccc 240
agaagtggcc gatcagccaa cgcctctgtc atccttaatg tgcaattcaa gccagagatt 300
gcccaagtgc gcgccaagta ccaggaagct caggggcccag gcctcctggg tgtcctgttt 360
10 gccctgggtgc gtgccaaccc gccggccaat gtcacctgga tcgaccagga tgggccagt 420
actgtcaaca cctctgactt cctgggtgctg gatgcgaga actaccctg gtcaccaac 480
cacacgggtgc agctgcagct ccgcagcctg gcacacaacc tctcggtggg ggccaccaat 540
gacgtgggtg tcaccagtgc gtcgcttcca gcccagggc ttctggctac ccgggtggaa 600
gtgccactgc tgggcattgt tgtggctgct gggcttgac tgggcaccct cgtgggggtc 660
15 agcaccttgg tggcctgcct ggtctgcaga aaagagaaga aaaccaaagg cccctcccgg 720
caccatctc tgatatcaag tgactccaac aacctaaaac tcaacaacgt gcgcctgcca 780
cgggagaaca tgtccctccc gtccaacctt cagctcaatg acctcactcc agattccaga 840
gcagtgaaac cagcagaccg gcagatggct cagaacaaca gccggccaga gcttctggac 900
ccggagcccc gcggcctcct caccagccaa gcatgtctcc tccaccaagg gacccagcc 960
20 ctgaccaacc catggttgcc tcatcagcag gaaggtgccc ttctggagg atggtcgcca 1020
caggcacata attcaacagt gtggaagctt tag 1053

<210> 106

<211> 342

25 <212> DNA

238/346

<213> Homo sapiens

<400> 106

atgaatgaga caaacaaaac acttggtggg ctttcggagc tccccacagc gtctgctgtg 60
5 gcccttggcc caggcactgg ggctcgggca tggcctgtgc tggtaggatt tgtgctgggg 120
gctgtggtcc tctcgtcctt cattgcactt gctgccaaat gccacctctg ccgccgatac 180
catgccagct accggcaccg ccactgcct gagacaggaa ggggaggccg cccacaggtg 240
gctgaagatg aggatgatga tggcttcacg gaggacaatt acattcagcc tgggactggc 300
gagctgggga cagagggtag cagggaaccac ttctccctct ga 342

10

<210> 107

<211> 570

<212> DNA

<213> Homo sapiens

15

<400> 107

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239/346

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570

<210> 108

<211> 834

5 <212> DNA

<213> Homo sapiens

<400> 108

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20 ctttcgctac atttcatgtg ttttgatgaa gcattccctc agttttttat agtatactgg 720
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<210> 109

25 <211> 825

240/346

<212> DNA

<213> Homo sapiens

<400> 109

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20 <210> 110

<211> 1173

<212> DNA

<213> Homo sapiens

25 <400> 110

241/346

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<210> 111

<211> 1894

<212> DNA

25 <213> Homo sapiens

242/346

<220>

<221> CDS

<222> (36)..(719)

5

<400> 111

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    Gly Pro Leu Arg Ala Met Gly Arg Gln Ala Leu Leu Leu Leu Ala Leu
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    tgc gcc aca ggc gcc cag ggg ctc tac ttc cac atc ggc gag acc gag      149
    Cys Ala Thr Gly Ala Gln Gly Leu Tyr Phe His Ile Gly Glu Thr Glu

15      25             30             35

    aag cgc tgt ttc atc gag gaa atc ccc gac gag acc atg gtc atc ggc      197
    Lys Arg Cys Phe Ile Glu Glu Ile Pro Asp Glu Thr Met Val Ile Gly

        40             45             50

    aac tat cgt acc cag atg tgg gat aag cag aag gag gtc ttc ctg ccc      245
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    55             60             65             70

    tcg acc cct ggc ctg ggc atg cac gtg gaa gtg aag gac ccc gac ggc      293
    Ser Thr Pro Gly Leu Gly Met His Val Glu Val Lys Asp Pro Asp Gly

        75             80             85

25  aag gtg gtg ctg tcc cgg cag tac ggc tcg gag ggc cgc ttc acg ttc      341

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				90					95					100			
	acc	tcc	cac	acg	ccc	ggt	gac	cat	caa	atc	tgt	ctg	cac	tcc	aat	tct	389
	Thr	Ser	His	Thr	Pro	Gly	Asp	His	Gln	Ile	Cys	Leu	His	Ser	Asn	Ser	
5			105						110					115			
	acc	agg	atg	gct	ctc	ttc	gct	ggt	ggc	aaa	ctg	cgg	gtg	cat	ctc	gac	437
	Thr	Arg	Met	Ala	Leu	Phe	Ala	Gly	Gly	Lys	Leu	Arg	Val	His	Leu	Asp	
			120						125					130			
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10	Ile	Gln	Val	Gly	Glu	His	Ala	Asn	Asn	Tyr	Pro	Glu	Ile	Ala	Ala	Lys	
			135						140					145		150	
	gat	aag	ctg	acg	gag	cta	cag	ctc	cgc	gcc	cgc	cag	ttg	ctt	gat	cag	533
	Asp	Lys	Leu	Thr	Glu	Leu	Gln	Leu	Arg	Ala	Arg	Gln	Leu	Leu	Asp	Gln	
				155					160					165			
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	Val	Glu	Gln	Ile	Gln	Lys	Glu	Gln	Asp	Tyr	Gln	Arg	Tyr	Arg	Glu	Glu	
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	cgc	ttc	cga	ctg	acg	agc	gag	agc	acc	aac	cag	agg	gtc	cta	tgg	tgg	629
	Arg	Phe	Arg	Leu	Thr	Ser	Glu	Ser	Thr	Asn	Gln	Arg	Val	Leu	Trp	Trp	
20			185						190					195			
	tcc	att	gct	cag	act	gtc	atc	ctc	atc	ctc	act	ggc	atc	tgg	cag	atg	677
	Ser	Ile	Ala	Gln	Thr	Val	Ile	Leu	Ile	Leu	Thr	Gly	Ile	Trp	Gln	Met	
			200						205					210			
	cgt	cac	ctc	aag	agc	ttc	ttt	gag	gcc	aag	aag	ctg	gtg	tag			719
25	Arg	His	Leu	Lys	Ser	Phe	Phe	Glu	Ala	Lys	Lys	Leu	Val				

244/346

215 220 225

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<210> 112

<211> 2413

25 <212> DNA

245/346

<213> Homo sapiens

<220>

<221> CDS

5 <222> (115)..(1173)

<400> 112

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10 Met
1
gag agc gga ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc 165
Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr
5 10 15
acc tct gtg gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc 213
Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala
20 25 30
cgg gtc tcc caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa 261
Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu
20 35 40 45
gat tta aag agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat 309
Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr
50 55 60 65
gct gtt ata gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc 357
25 Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser
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	Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln			
	85	90	95	
5	gag cac aag atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc			453
	Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys			
	100	105	110	
	tca aag atc att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg			501
	Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val			
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	ccc cac gag gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg			549
	Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu			
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	gac tca gtg gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc			597
15	Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro			
	150	155	160	
	tcg att cag tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag			645
	Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu			
	165	170	175	
20	cgg ccc aaa ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc			693
	Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala			
	180	185	190	
	acc ctc aca ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc			741
	Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg			
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	ttc gac agc ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag	837
5	Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys	
	230 235 240	
	gtg ctg gcg ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc	885
	Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe	
	245 250 255	
10	att ctc cgg aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag	933
	Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys	
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	Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg	
15	275 280 285	
	gcc aag cct gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt	1029
	Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys	
	290 295 300 305	
	ctg agc agc ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt	1077
20	Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys	
	310 315 320	
	tcc tgc acc gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct	1125
	Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro	
	325 330 335	
25	atc tgc aga cag gcg atc acc cgg gtg ata ccc ctg tac aac agc taa	1173

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340

345

350

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249/346

<211> 2376

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (35)..(427)

<400> 113

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Pro Gly Ala Ser Ala Ser Ser Ala Pro Pro Ala Gln Glu Glu Gly Met

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Thr Trp Trp Tyr Arg Trp Leu Cys Arg Leu Ser Gly Val Leu Gly Ala

25 30 35
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20 Val Ser Cys Ala Ile Ser Gly Leu Phe Asn Cys Ile Thr Ile His Pro

40 45 50 55
ctg aac atc gcg gcc ggc gtg tgg atg atg atg gcg gtc gtt ccc atc 247
Leu Asn Ile Ala Ala Gly Val Trp Met Met Met Ala Val Val Pro Ile

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 Ala Thr Gly Val Leu Tyr Gly Leu Ser Ala Leu Gly Lys Lys Gly Asp
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 Ala Ile Ser Tyr Ala Arg Ile Gln Gln Gln Arg Gln Gln Ala Asp Glu
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aggctgcccc tgtaccctgt ggggaaatgg tgggtgcatg gctggatgca gaggtggaag 2117
15 gccctgggcc acaggcgaga gtgggcgtgt cacctgtccc aggttcccag caagtctgca 2177
gctgtgcagt cctgggggtc ctgacctgt cggccagggt gcgtgctgtc cagcaggggc 2237
cctgccttgc aaggaacgtc tcttcggcg gctgggccgc tcctgcctgg tctgggctgt 2297
gtgtggcgcc ctttctcct tgtttgttc tctgtgttct gtgtgctct taagcaataa 2357
agcgtggccg tggctcgcg 2376

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<211> 1155

<212> DNA

<213> Homo sapiens

25

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<220>

<221> CDS

<222> (110)..(1102)

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gcagcgcccg cgtagatcgc ttcggccggg ttctacgccc ggctcaact atg agc cgg 118

Met Ser Arg

1

10 tgc gcc cag gcg gcg gaa gtg gcg gcc aca gtg cca ggt gcc ggc gtc 166
Cys Ala Gln Ala Ala Glu Val Ala Ala Thr Val Pro Gly Ala Gly Val

5

10

15

ggg aac gtg ggg ctg cgg ccg ccc atg gtg ccc cgt cag gcg tcc ttc 214
Gly Asn Val Gly Leu Arg Pro Pro Met Val Pro Arg Gln Ala Ser Phe

15 20 25 30 35

ttc ccg ccg ccg gtg ccg aac ccc ttc gtg cag cag acg cag atc ggc 262
Phe Pro Pro Pro Val Pro Asn Pro Phe Val Gln Gln Thr Gln Ile Gly

40

45

50

tcc gcg agg cgg gtc cag att gtc ctt ctt ggg att atc ttg ctt cca 310

20 Ser Ala Arg Arg Val Gln Ile Val Leu Leu Gly Ile Ile Leu Leu Pro

55

60

65

att cgt gtc tta ttg gtt gcg tta att tta tta ctt gca tgg cca ttt 358
Ile Arg Val Leu Leu Val Ala Leu Ile Leu Leu Leu Ala Trp Pro Phe

70

75

80

25 gct gca att tca aca gta tgc tgt cct gaa aag ctg acc cac cca ata 406

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	Ala	Ala	Ile	Ser	Thr	Val	Cys	Cys	Pro	Glu	Lys	Leu	Thr	His	Pro	Ile	
	85						90					95					
	act	ggt	tgg	agg	agg	aaa	att	act	caa	aca	gct	ttg	aaa	ttt	ctg	ggt	454
	Thr	Gly	Trp	Arg	Arg	Lys	Ile	Thr	Gln	Thr	Ala	Leu	Lys	Phe	Leu	Gly	
5	100					105					110			115			
	cgt	gct	atg	ttc	ttt	tca	atg	gga	ttt	ata	gtt	gct	gta	aaa	gga	aag	502
	Arg	Ala	Met	Phe	Phe	Ser	Met	Gly	Phe	Ile	Val	Ala	Val	Lys	Gly	Lys	
						120					125			130			
	att	gca	agt	cct	ttg	gaa	gca	cca	gtt	ttt	gtt	gct	gcc	cct	cat	tca	550
10	Ile	Ala	Ser	Pro	Leu	Glu	Ala	Pro	Val	Phe	Val	Ala	Ala	Pro	His	Ser	
						135					140			145			
	aca	ttc	ttt	gat	gga	att	gcc	tgt	gtt	gta	gct	ggg	tta	cct	tct	ata	598
	Thr	Phe	Phe	Asp	Gly	Ile	Ala	Cys	Val	Val	Ala	Gly	Leu	Pro	Ser	Ile	
						150					155			160			
15	gta	tct	cga	aat	gag	aat	gca	caa	gtc	cct	ctg	att	ggc	aga	ctg	tta	646
	Val	Ser	Arg	Asn	Glu	Asn	Ala	Gln	Val	Pro	Leu	Ile	Gly	Arg	Leu	Leu	
						165					170			175			
	cgg	gct	gtg	caa	cca	gtt	ttg	gtg	tcc	cgt	gta	gat	ccg	gat	tcc	cga	694
	Arg	Ala	Val	Gln	Pro	Val	Leu	Val	Ser	Arg	Val	Asp	Pro	Asp	Ser	Arg	
20	180					185					190			195			
	aaa	aac	aca	ata	aat	gaa	ata	ata	aag	cga	aca	aca	tca	gga	gga	gaa	742
	Lys	Asn	Thr	Ile	Asn	Glu	Ile	Ile	Lys	Arg	Thr	Thr	Ser	Gly	Gly	Glu	
						200					205			210			
	tgg	ccc	cag	ata	cta	gtt	ttc	cca	gaa	ggt	act	tgt	act	aat	cgt	tcc	790
25	Trp	Pro	Gln	Ile	Leu	Val	Phe	Pro	Glu	Gly	Thr	Cys	Thr	Asn	Arg	Ser	

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	215	220	225	
	tgt ttg att act ttt aaa cca gga gcc ttc att cca gga gtt cca gtg			838
	Cys Leu Ile Thr Phe Lys Pro Gly Ala Phe Ile Pro Gly Val Pro Val			
	230	235	240	
5	cag cca gtc ctc ctc aga tac cca aac aag ctg gat act gtg acc tgg			886
	Gln Pro Val Leu Leu Arg Tyr Pro Asn Lys Leu Asp Thr Val Thr Trp			
	245	250	255	
	aca tgg caa gga tat aca ttc att cag ctt tgt atg ctt act ttc tgc			934
	Thr Trp Gln Gly Tyr Thr Phe Ile Gln Leu Cys Met Leu Thr Phe Cys			
10	260	265	270	275
	cag ctc ttc aca aag gta gaa gtt gag atg ttt ctg ttc ttt tgg gaa			982
	Gln Leu Phe Thr Lys Val Glu Val Glu Met Phe Leu Phe Phe Trp Glu			
	280	285	290	
	gga agc agc aag cat tgt tta aaa ata tct tcc ttc ttt tgc att ttt			1030
15	Gly Ser Ser Lys His Cys Leu Lys Ile Ser Ser Phe Phe Cys Ile Phe			
	295	300	305	
	tct ctt cga aga ttt aaa aga aga att aca caa aga act aga act gca			1078
	Ser Leu Arg Arg Phe Lys Arg Arg Ile Thr Gln Arg Thr Arg Thr Ala			
	310	315	320	
20	cat ttg tta aga ttg tcc ttt taa aattattttc tggtacaagg aaaaaataaa			1132
	His Leu Leu Arg Leu Ser Phe			
	325	330		
	agattgatta tagtgatcata att			1155
25	<210> 115			

255/346

<211> 1329

<212> DNA

<213> Homo sapiens

5 <220>

<221> CDS

<222> (71)..(1123)

<400> 115

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Met Ala Leu Pro Pro Gly Pro Ala Ala Leu Arg His Thr
1 5 10
ctg ctg ctc ctg cca gcc ctt ctg agc tca ggt ggg cct ggc acc ccc 157
15 Leu Leu Leu Leu Pro Ala Leu Leu Ser Ser Gly Gly Pro Gly Thr Pro
15 20 25
aga ttg gcc tgg tat ctg gat gga cag ctg cag gag gcc agc acc tca 205
Arg Leu Ala Trp Tyr Leu Asp Gly Gln Leu Gln Glu Ala Ser Thr Ser
30 35 40 45
20 aga ctg ctg agc gtg gga ggg gag gcc ttc tct gga ggc acc agc acc 253
Arg Leu Leu Ser Val Gly Gly Glu Ala Phe Ser Gly Gly Thr Ser Thr
50 55 60
ttc act gtc act gcc cat cgg gcc cag cat gag ctc aac tgc tct ctg 301
Phe Thr Val Thr Ala His Arg Ala Gln His Glu Leu Asn Cys Ser Leu
25 65 70 75

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	cag gac ccc aga agt ggc cga tca gcc aac gcc tct gtc atc ctt aat	349
	Gln Asp Pro Arg Ser Gly Arg Ser Ala Asn Ala Ser Val Ile Leu Asn	
	80 85 90	
	gtg caa ttc aag cca gag att gcc caa gtc ggc gcc aag tac cag gaa	397
5	Val Gln Phe Lys Pro Glu Ile Ala Gln Val Gly Ala Lys Tyr Gln Glu	
	95 100 105	
	gct cag ggc cca ggc ctc ctg gtt gtc ctg ttt gcc ctg gtg cgt gcc	445
	Ala Gln Gly Pro Gly Leu Leu Val Val Leu Phe Ala Leu Val Arg Ala	
	110 115 120 125	
10	aac ccg ccg gcc aat gtc acc tgg atc gac cag gat ggg cca gtg act	493
	Asn Pro Pro Ala Asn Val Thr Trp Ile Asp Gln Asp Gly Pro Val Thr	
	130 135 140	
	gtc aac acc tct gac ttc ctg gtg ctg gat gcg cag aac tac ccc tgg	541
	Val Asn Thr Ser Asp Phe Leu Val Leu Asp Ala Gln Asn Tyr Pro Trp	
15	145 150 155	
	ctc acc aac cac acg gtg cag ctg cag ctc cgc agc ctg gca cac aac	589
	Leu Thr Asn His Thr Val Gln Leu Gln Leu Arg Ser Leu Ala His Asn	
	160 165 170	
	ctc tcg gtg gtg gcc acc aat gac gtg ggt gtc acc agt gcg tcg ctt	637
20	Leu Ser Val Val Ala Thr Asn Asp Val Gly Val Thr Ser Ala Ser Leu	
	175 180 185	
	cca gcc cca ggg ctt ctg gct acc cgg gtg gaa gtg cca ctg ctg ggc	685
	Pro Ala Pro Gly Leu Leu Ala Thr Arg Val Glu Val Pro Leu Leu Gly	
	190 195 200 205	
25	att gtt gtg gct gct ggg ctt gca ctg ggc acc ctc gtg ggg ttc agc	733

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Ile Val Val Ala Ala Gly Leu Ala Leu Gly Thr Leu Val Gly Phe Ser
210 215 220
acc ttg gtg gcc tgc ctg gtc tgc aga aaa gag aag aaa acc aaa ggc 781
Thr Leu Val Ala Cys Leu Val Cys Arg Lys Glu Lys Lys Thr Lys Gly
5 225 230 235
ccc tcc cgg cac cca tct ctg ata tca agt gac tcc aac aac cta aaa 829
Pro Ser Arg His Pro Ser Leu Ile Ser Ser Asp Ser Asn Asn Leu Lys
240 245 250
ctc aac aac gtg cgc ctg cca cgg gag aac atg tcc ctc ccg tcc aac 877
10 Leu Asn Asn Val Arg Leu Pro Arg Glu Asn Met Ser Leu Pro Ser Asn
255 260 265
ctt cag ctc aat gac ctc act cca gat tcc aga gca gtg aaa cca gca 925
Leu Gln Leu Asn Asp Leu Thr Pro Asp Ser Arg Ala Val Lys Pro Ala
270 275 280 285
15 gac cgg cag atg gct cag aac aac agc cgg cca gag ctt ctg gac ccg 973
Asp Arg Gln Met Ala Gln Asn Asn Ser Arg Pro Glu Leu Leu Asp Pro
290 295 300
gag ccc ggc ggc ctc ctc acc agc caa gca tgt ctc ctc cac cac ggg 1021
Glu Pro Gly Gly Leu Leu Thr Ser Gln Ala Cys Leu Leu His His Gly
20 305 310 315
acc cca gcc ctg acc aac cca tgg ttg cct cat cag cag gaa ggt gcc 1069
Thr Pro Ala Leu Thr Asn Pro Trp Leu Pro His Gln Gln Glu Gly Ala
320 325 330
ctt cct gga gga tgg tcg cca cag gca cat aat tca aca gtg tgg aag 1117
25 Leu Pro Gly Gly Trp Ser Pro Gln Ala His Asn Ser Thr Val Trp Lys

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335 340 345

ctt tag gggaacatgg agaaagaagg agaccacata ccccaaagtg acctaagaac 1173
Leu

350

5 actttaaaaa gcaacatgta aatgattgga aattaatata gtacagaata tattttttccc 1233
ttgttgagat cttcttttgt aatgtttttc atgttactgc ctagggcggg gctgagcaca 1293
cagcaagttt aataaacttg actgaattca tttaat 1329

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10 <211> 1387

<212> DNA

<213> Homo sapiens

<220>

15 <221> CDS

<222> (147)..(488)

<400> 116

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20 ggggctgcct ggcattctggg ggcctcctca gagccagggc tctttctggt tgaggctgag 120
actcactggt gtcattcaggc ccctcc atg aat gag aca aac aaa aca ctt gtt 173

Met Asn Glu Thr Asn Lys Thr Leu Val

1 5

ggg cct tcg gag ctc ccc aca gcg tct gct gtg gcc cct ggc cca ggc 221

25 Gly Pro Ser Glu Leu Pro Thr Ala Ser Ala Val Ala Pro Gly Pro Gly

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	10	15	20	25	
	act ggg gct cgg gca tgg cct gtg ctg gta gga ttt gtg ctg ggg gct				269
	Thr Gly Ala Arg Ala Trp Pro Val Leu Val Gly Phe Val Leu Gly Ala				
	30	35	40		
5	gtg gtc ctc tcg ctc ctc att gca ctt gct gcc aaa tgc cac ctc tgc				317
	Val Val Leu Ser Leu Leu Ile Ala Leu Ala Ala Lys Cys His Leu Cys				
	45	50	55		
	cgc cga tac cat gcc agc tac cgg cac cgc cca ctg cct gag aca gga				365
	Arg Arg Tyr His Ala Ser Tyr Arg His Arg Pro Leu Pro Glu Thr Gly				
10	60	65	70		
	agg gga ggc cgc cca cag gtg gct gaa gat gag gat gat gat ggc ttc				413
	Arg Gly Gly Arg Pro Gln Val Ala Glu Asp Glu Asp Asp Asp Gly Phe				
	75	80	85		
	atc gag gac aat tac att cag cct ggg act ggc gag ctg ggg aca gag				461
15	Ile Glu Asp Asn Tyr Ile Gln Pro Gly Thr Gly Glu Leu Gly Thr Glu				
	90	95	100	105	
	ggg agc agg gac cac ttc tcc ctc tga gctcccatct ttagaccctc				508
	Gly Ser Arg Asp His Phe Ser Leu				
	110				
20	cccactccct ccatgcctga cagcttaagg acagtgggta tgacatgggg gccttgaacc				568
	tcagggacag aggtggctgg ggcttaaagg ttggccaggg atggagtaaa cccacttcc				628
	ctgacactag ccagcaaagt gacaatgacc ctctcttgct caataactct caactgttcc				688
	ctgctgttct caggataaag ccaaacaaag gcttgagtgt ggacataagg ccctctgtga				748
	tcatgcctct cggcctcttg gtttcttttc ttgccttccc ctactttact gtcgaaatca				808
25	atgctattct ccctcccacc acttcccatg cagtttcccc aggcaccttt gtcacattg				868

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<211> 1158
<212> DNA
<213> Homo sapiens

15

<220>
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<222> (130)..(699)

20

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tcctggggac tctgtgggga cgcgccccgc gccgcggctc ggggaccggt agagcccggc 120
gctgcgcgc atg gcc ctg ctc tcg cgc ccc gcg ctc acc ctc ctg ctc ctc 171

Met Ala Leu Leu Ser Arg Pro Ala Leu Thr Leu Leu Leu Leu

25

1

5

10

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ctc atg gcc gct gtt gtc agg tgc cag gag cag gcc cag acc acc gac 219
Leu Met Ala Ala Val Val Arg Cys Gln Glu Gln Ala Gln Thr Thr Asp
15          20          25          30
tgg aga gcc acc ctg aag acc atc cgg aac ggc gtt cat aag ata gac 267
5 Trp Arg Ala Thr Leu Lys Thr Ile Arg Asn Gly Val His Lys Ile Asp
          35          40          45
acg tac ctg aac gcc gcc ttg gac ctc ctg gga ggc gag gac ggt ctc 315
Thr Tyr Leu Asn Ala Ala Leu Asp Leu Leu Gly Gly Glu Asp Gly Leu
          50          55          60
10 tgc cag tat aaa tgc agt gac gga tct aag cct ttc cca cgt tat ggt 363
Cys Gln Tyr Lys Cys Ser Asp Gly Ser Lys Pro Phe Pro Arg Tyr Gly
          65          70          75
tat aaa ccc tcc cca ccg aat gga tgt ggc tct cca ctg ttt ggt gtt 411
Tyr Lys Pro Ser Pro Pro Asn Gly Cys Gly Ser Pro Leu Phe Gly Val
15          80          85          90
cat ctt aac att ggt atc cct tcc ctg aca aag tgt tgc aac caa cac 459
His Leu Asn Ile Gly Ile Pro Ser Leu Thr Lys Cys Cys Asn Gln His
          95          100          105          110
gac agg tgc tat gaa acc tgt ggc aaa agc aag aat gac tgt gat gaa 507
20 Asp Arg Cys Tyr Glu Thr Cys Gly Lys Ser Lys Asn Asp Cys Asp Glu
          115          120          125
gaa ttc cag tat tgc ctc tcc aag atc tgc cga gat gta cag aaa aca 555
Glu Phe Gln Tyr Cys Leu Ser Lys Ile Cys Arg Asp Val Gln Lys Thr
          130          135          140
25 cta gga cta act cag cat gtt cag gca tgt gaa aca aca gtg gag ctc 603

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Leu Gly Leu Thr Gln His Val Gln Ala Cys Glu Thr Thr Val Glu Leu
145 150 155

ttg ttt gac agt gtt ata cat tta ggt tgt aaa cca tat ctg gac agc 651
Leu Phe Asp Ser Val Ile His Leu Gly Cys Lys Pro Tyr Leu Asp Ser
5 160 165 170

caa cga gcc gca tgc agg tgt cat tat gaa gaa aaa act gat ctt taa 699
Gln Arg Ala Ala Cys Arg Cys His Tyr Glu Glu Lys Thr Asp Leu
175 180 185 190

aggagatgcc gacagctagt gacagatgaa gatggaagaa cataaccttt gacaaataac 759
10 taatgtttttt acaacataaa actgtcttat ttttgtgaaa ggattatttt gagaccttaa 819
aataatttat atcttgatgt taaaacctca aagcaaaaaa agtgagggag atagtgaggg 879
gagggcacgc ttgtcttctc aggtatcttc ccagcattg ctcccttact tagtatgcca 939
aatgtcttga ccaatatcaa aaacaagtgc ttgttttagcg gagaattttg aaaagaggaa 999
tatataactc aattttcaca accacattta ccaaaaaaag agatcaaata taaaattcat 1059
15 cataatgtct gttcaacatt atcttatttg gaaaatgggg aaattatcac ttacaagtat 1119
ttgtttacta tgaaatttta aatacacatt tatgcctag 1158

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20 <212> DNA
<213> Homo sapiens

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<221> CDS
25 <222> (26)..(859)

263/346

<400> 118

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                                Met Ser Pro Leu Leu Gly Leu Arg Ser
5                                1                                5

gag ctg cag gac acc tgc acc tcg ctg gga ctg atg ctg tcg gtg gtg 100
Glu Leu Gln Asp Thr Cys Thr Ser Leu Gly Leu Met Leu Ser Val Val
10                                15                                20                                25

ctg ctc atg ggg ctg gcc cgc gta gtc gcc cgg cag cag ctg cac agg 148
Leu Leu Met Gly Leu Ala Arg Val Val Ala Arg Gln Gln Leu His Arg
30                                35                                40

ccg gtg gcc cac gcc ttc gtc ctg gag ttt cta gcc acc ttc cag ctc 196
Pro Val Ala His Ala Phe Val Leu Glu Phe Leu Ala Thr Phe Gln Leu
45                                50                                55

15 tgc tgc tgc acc cac gag ctg caa ctg ctg agc gaa cag cac ccc gcg 244
Cys Cys Cys Thr His Glu Leu Gln Leu Leu Ser Glu Gln His Pro Ala
60                                65                                70

cac ccc acc tgg acg ctg acg ctc gtc tac ttc ttc tcg ctt gtg cat 292
His Pro Thr Trp Thr Leu Thr Leu Val Tyr Phe Phe Ser Leu Val His
20 75                                80                                85

ggc ctg act ctg gtg ggc acg tcc agc aac ccg tgc ggc gtg atg atg 340
Gly Leu Thr Leu Val Gly Thr Ser Ser Asn Pro Cys Gly Val Met Met
90                                95                                100                                105

cag atg atg ctg ggg ggc atg tcc ccc gag acg ggt gcg gtg agg cta 388
25 Gln Met Met Leu Gly Gly Met Ser Pro Glu Thr Gly Ala Val Arg Leu

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	110	115	120	
	ttg gct cag ctg gtt agt gcc ctg tgc agc agg tac tgc aca agc gcc	436		
	Leu Ala Gln Leu Val Ser Ala Leu Cys Ser Arg Tyr Cys Thr Ser Ala			
	125	130	135	
5	ttg tgg agc ttg ggt ctg acc cag tat cac gtc agc gag agg agc ttc	484		
	Leu Trp Ser Leu Gly Leu Thr Gln Tyr His Val Ser Glu Arg Ser Phe			
	140	145	150	
	gct tgc aag aat ccc atc cga gtc gac ttg ctc aaa gcg gtc atc aca	532		
	Ala Cys Lys Asn Pro Ile Arg Val Asp Leu Leu Lys Ala Val Ile Thr			
10	155	160	165	
	gag gcc gtc tgc tcc ttt ctc ttc cac agc gct ctg ctg cac ttc cag	580		
	Glu Ala Val Cys Ser Phe Leu Phe His Ser Ala Leu Leu His Phe Gln			
	170	175	180	185
	gaa gtc cga acc aag ctt cgt atc cac ctg ctg gct gca ctc atc acc	628		
15	Glu Val Arg Thr Lys Leu Arg Ile His Leu Leu Ala Ala Leu Ile Thr			
	190	195	200	
	ttt ttg gtc tat gca gga gga agt cta aca gga gct gta ttt aat cca	676		
	Phe Leu Val Tyr Ala Gly Gly Ser Leu Thr Gly Ala Val Phe Asn Pro			
	205	210	215	
20	gct ttg gca ctt tcg cta cat ttc atg tgt ttt gat gaa gca ttc cct	724		
	Ala Leu Ala Leu Ser Leu His Phe Met Cys Phe Asp Glu Ala Phe Pro			
	220	225	230	
	cag ttt ttt ata gta tac tgg ctg gct cct tct tta ggt ata ttg ttg	772		
	Gln Phe Phe Ile Val Tyr Trp Leu Ala Pro Ser Leu Gly Ile Leu Leu			
25	235	240	245	

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atg att ttg atg ttc agc ttt ttc cat ggc tgc ata aca acc ata caa 820
Met Ile Leu Met Phe Ser Phe Phe His Gly Cys Ile Thr Thr Ile Gln
250 255 260 265
tta ata aaa agg aat aac tgt tcc aaa gac tca gac taa catacaggac 869
5 Leu Ile Lys Arg Asn Asn Cys Ser Lys Asp Ser Asp
270 275
agtccagctg gatgtgataa agatTTTTatc acctcatatg gaaaacaccg gctgcactgg 929
attcatcagt gttaacttcc ttgaggaag ctgcottata gttttcatca ctgggacttt 989
aaaaaaaaat tactgtgaaa atgaggtatt ctgtacttct cagttaagac ttgttctttg 1049
10 agtgatgtat taaatgctgc tagaaaagcc tcattacatt aaatataaat caatctt 1106

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<211> 1907
<212> DNA
15 <213> Homo sapiens

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<222> (159)..(983)
20

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ccaccccccg gctcccgga ctgtggactc cacgacctg tcctcgggcc tgtccgcgcc 120
gaagcagccc gggactgcgc agcgccccgc gtgccgac atg gga aag tct ctt tct 176
25 Met Gly Lys Ser Leu Ser

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		1	5	
	cat ttg cct ttg cat tca agc aaa gaa gat gct tat gat gga gtc aca	224		
	His Leu Pro Leu His Ser Ser Lys Glu Asp Ala Tyr Asp Gly Val Thr			
	10 15 20			
5	tct gaa aac atg agg aat gga ctg gtt aat agt gaa gtc cat aat gaa	272		
	Ser Glu Asn Met Arg Asn Gly Leu Val Asn Ser Glu Val His Asn Glu			
	25 30 35			
	gat gga aga aat gga gat gtc tct cag ttt cca tat gtg gaa ttt aca	320		
	Asp Gly Arg Asn Gly Asp Val Ser Gln Phe Pro Tyr Val Glu Phe Thr			
10	40 45 50			
	gga aga gat agt gtc acc tgc cct act tgt cag gga aca gga aga att	368		
	Gly Arg Asp Ser Val Thr Cys Pro Thr Cys Gln Gly Thr Gly Arg Ile			
	55 60 65 70			
	cct agg ggg caa gaa aac caa ctg gtg gca ttg att cca tat agt gat	416		
15	Pro Arg Gly Gln Glu Asn Gln Leu Val Ala Leu Ile Pro Tyr Ser Asp			
	75 80 85			
	cag aga tta agg cca aga aga aca aag ctg tat gtg atg gct tct gtg	464		
	Gln Arg Leu Arg Pro Arg Arg Thr Lys Leu Tyr Val Met Ala Ser Val			
	90 95 100			
20	ttt gtc tgt cta ctc ctt tct gga ttg gct gtg ttt ttc ctt ttc cct	512		
	Phe Val Cys Leu Leu Leu Ser Gly Leu Ala Val Phe Phe Leu Phe Pro			
	105 110 115			
	cgc tct atc gac gtg aaa tac att ggt gta aaa tca gcc tat gtc agt	560		
	Arg Ser Ile Asp Val Lys Tyr Ile Gly Val Lys Ser Ala Tyr Val Ser			
25	120 125 130			

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	tat gat gtt cag aag cgt aca att tat tta aat atc aca aac aca cta	608
	Tyr Asp Val Gln Lys Arg Thr Ile Tyr Leu Asn Ile Thr Asn Thr Leu	
	135 140 145 150	
	aat ata aca aac aat aac tat tac tct gtc gaa gtt gaa aac atc act	656
5	Asn Ile Thr Asn Asn Asn Tyr Tyr Ser Val Glu Val Glu Asn Ile Thr	
	155 160 165	
	gcc caa gtt caa ttt tca aaa aca gtt att gga aag gca cgc tta aac	704
	Ala Gln Val Gln Phe Ser Lys Thr Val Ile Gly Lys Ala Arg Leu Asn	
	170 175 180	
10	aac ata acc att att ggt cca ctt gat atg aaa caa att gat tac aca	752
	Asn Ile Thr Ile Ile Gly Pro Leu Asp Met Lys Gln Ile Asp Tyr Thr	
	185 190 195	
	gta cct acc gtt ata gca gag gaa atg agt tat atg tat gat ttc tgt	800
	Val Pro Thr Val Ile Ala Glu Glu Met Ser Tyr Met Tyr Asp Phe Cys	
15	200 205 210	
	act ctg ata tcc atc aaa gtg cat aac ata gta ctc atg atg caa gtt	848
	Thr Leu Ile Ser Ile Lys Val His Asn Ile Val Leu Met Met Gln Val	
	215 220 225 230	
	act gtg aca aca aca tac ttt ggc cac tct gaa cag ata tcc cag gag	896
20	Thr Val Thr Thr Thr Tyr Phe Gly His Ser Glu Gln Ile Ser Gln Glu	
	235 240 245	
	agg tat cag tat gtc gac tgt gga aga aac aca act tat cag ttg ggg	944
	Arg Tyr Gln Tyr Val Asp Cys Gly Arg Asn Thr Thr Tyr Gln Leu Gly	
	250 255 260	
25	cag tct gaa tat tta aat gta ctt cag cca caa cag taa aaactggaag	993

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Gln Ser Glu Tyr Leu Asn Val Leu Gln Pro Gln Gln

265

270

275

agatggattt aaagaagaaa tatctattga tatttcctat actctcaatg aagaggtatt 1053
 tcctaatagg agaccttaaa ttgaacaaac cttaaagtta cacttctaag agtacagtta 1113
 5 aaagtatgtg gacctgcagt tcttgtaact ctccactctg tgttaatgat atatttgtac 1173
 taggatcttt tacttgaatc taaatttact gggtgatttc cttctccagc ctatccccta 1233
 cagggaaaag ctgatacttc ccctatagta caataaataa ttatttaaaa gtcatagctc 1293
 cagtcactac tgaaaacata attttggtga taaaataatt tgagaaactt aatttctgaa 1353
 tgtttttata gaaaattact gaaagtctat tactcatgga agacttttaa agaataacct 1413
 10 tttttcctgt ttataaatt ccattgtta tatggtagta tttcagctac acaatatttt 1473
 agcttttagc tagacattta tagcttttca tttggtgaaa tggtaatcat ctgcatgttt 1533
 ttgtcactta tttcagggtta gtgattgcct aacacttata agccaaaata atctttgcaa 1593
 aattccatac ctaaaatttt gaaagcccct aatgttttca cacatctttc tgtattagtt 1653
 atagttttgt gaaatctttg tgtgatcttc aaacattatc atttaatgta caatactgta 1713
 15 aataaactgt gcatggcttt tatacagctt tagtaaagt caaataaagt ggtacagact 1773
 cattacaaca agtttctcat aaaaatacaa taaataggaa aatgaaattc agaaacccat 1833
 agactgggaa taggttccag ttacagcttg gatctggcat aaaataaatt tgaataaaaa 1893
 tattttgatg ctcc 1907

- 20 <210> 120
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 25 <220>

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<221> CDS

<222> (134)..(1306)

<400> 120

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    gccagggagg gcc atg att tcc ctg ccg ggg ccc ctg gtg acc aac ttg 169
          Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu
                1             5             10
10  ctg cgg ttt ttg ttc ctg ggg ctg agt gcc ctg gcg ccc ccc tcg cgg 217
    Leu Arg Phe Leu Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg
                15             20             25
    gcc cag ctg caa ctg cac ttg ccc gcc aac cgg ttg cag gcg gtg gag 265
    Ala Gln Leu Gln Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu
15      30             35             40
    gga ggg gaa gtg gtg ctt cca gcg tgg tac acc ttg cac ggg gag gtg 313
    Gly Gly Glu Val Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val
        45             50             55             60
    tct tca tcc cag cca tgg gag gtg ccc ttt gtg atg tgg ttc ttc aaa 361
20  Ser Ser Ser Gln Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys
                65             70             75
    cag aaa gaa aag gag gat cag gtg ttg tcc tac atc aat ggg gtc aca 409
    Gln Lys Glu Lys Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr
                80             85             90
25  aca agc aaa cct gga gta tcc ttg gtc tac tcc atg ccc tcc cgg aac 457

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Thr Ser Lys Pro Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn
 95 100 105
 ctg tcc ctg cgg ctg gag ggt ctc cag gag aaa gac tct ggc ccc tac 505
 Leu Ser Leu Arg Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr
 5 110 115 120
 agc tgc tcc gtg aat gtg caa gac aaa caa ggc aaa tct agg ggc cac 553
 Ser Cys Ser Val Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His
 125 130 135 140
 agc atc aaa acc tta gaa ctc aat gta ctg gtt cct cca gct cct cca 601
 10 Ser Ile Lys Thr Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro
 145 150 155
 tcc tgc cgt ctc cag ggt gtg ccc cat gtg ggg gca aac gtg acc ctg 649
 Ser Cys Arg Leu Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu
 160 165 170
 15 agc tgc cag tct cca agg agt aag ccc gct gtc caa tac cag tgg gat 697
 Ser Cys Gln Ser Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp
 175 180 185
 cgg cag ctt cca tcc ttc cag act ttc ttt gca cca gca tta gat gtc 745
 Arg Gln Leu Pro Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val
 20 190 195 200
 atc cgt ggg tct tta agc ctc acc aac ctt tcg tct tcc atg gct gga 793
 Ile Arg Gly Ser Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly
 205 210 215 220
 gtc tat gtc tgc aag gcc cac aat gag gtg ggc act gcc caa tgt aat 841
 25 Val Tyr Val Cys Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn

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	225	230	235	
	gtg acg ctg gaa gtg agc aca ggg cct gga gct gca gtg gtt gct gga	889		
	Val Thr Leu Glu Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly			
	240	245	250	
5	gct gtt gtg ggt acc ctg gtt gga ctg ggg ttg ctg gct ggg ctg gtc	937		
	Ala Val Val Gly Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val			
	255	260	265	
	ctc ttg tac cac tgc cgg ggc aag gcc ctg gag gag cca gcc aat gat	985		
	Leu Leu Tyr His Cys Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp			
10	270	275	280	
	atc aag gag gat gcc att gct ccc cgg acc ctg ccc tgg ccc aag agc	1033		
	Ile Lys Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser			
	285	290	295	300
	tca gac aca atc tcc aag aat ggg acc ctt tcc tct gtc acc tcc gca	1081		
15	Ser Asp Thr Ile Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala			
	305	310	315	
	cga gcc ctc cgg cca ccc cat ggc cct ccc agg cct ggt gca ttg acc	1129		
	Arg Ala Leu Arg Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr			
	320	325	330	
20	ccc acg ccc agt ctc tcc agc cag gcc ctg ccc tca cca aga ctg ccc	1177		
	Pro Thr Pro Ser Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro			
	335	340	345	
	acg aca gat ggg gcc cac cct caa cca ata tcc ccc atc cct ggt ggg	1225		
	Thr Thr Asp Gly Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly			
25	350	355	360	

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gtt tct tcc tct ggc ttg agc cgc atg ggt gct gtg cct gtg atg gtg 1273
Val Ser Ser Ser Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val
365 370 375 380
cct gcc cag agt caa gct ggc tct ctg gta tga tgaccccacc actcattggc 1326
5 Pro Ala Gln Ser Gln Ala Gly Ser Leu Val
385 390
taaaggattt ggggtctctc cttcctatag gggtcacctc tagcacagag gcctgagtca 1386
tgaggaaagag tcacactcct gacccttagt actctgcccc cacctctctt tactgtggga 1446
aaaccatctc agtaagacct aagtgtccag gagacagaag gagaagagga agtggatctg 1506
10 gaattgggag gagcctccac ccaccctga ctctcctta tgaagccagc tgctgaaatt 1566
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15 tgtttgtatg 1816

<210> 121
<211> 395
<212> PRT
20 <213> Homo sapiens

<400> 121
Met Ser Gly Met Glu Glu Tyr Thr Thr Val Ser Gly Glu Val Leu Gln
1 5 10 15
25 Arg Trp Lys Ile Pro Ser Phe Lys Glu Asn Gln Thr Leu Ser Met Gly

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	20	25	30
	Ala Ala Thr Val Gln Ser Arg Gly Gln Tyr Ser Cys Ser Gly Gln Val		
	35	40	45
	Met Tyr Ile Pro Gln Thr Phe Thr Gln Thr Ser Glu Thr Ala Met Val		
5	50	55	60
	Gln Val Gln Glu Leu Phe Pro Pro Pro Val Leu Ser Ala Ile Pro Ser		
	65	70	75
	Pro Glu Pro Arg Glu Gly Ser Leu Val Thr Leu Arg Cys Gln Thr Lys		
	85	90	95
10	Leu His Pro Leu Arg Ser Ala Leu Arg Leu Leu Phe Ser Phe His Lys		
	100	105	110
	Asp Gly His Thr Leu Gln Asp Arg Gly Pro His Pro Glu Leu Cys Ile		
	115	120	125
	Pro Gly Ala Lys Glu Gly Asp Ser Gly Leu Tyr Trp Cys Glu Val Ala		
15	130	135	140
	Pro Glu Gly Gly Gln Val Gln Lys Gln Ser Pro Gln Leu Glu Val Arg		
	145	150	155
	Val Gln Ala Pro Val Ser Arg Pro Val Leu Thr Leu His His Gly Pro		
	165	170	175
20	Ala Asp Pro Ala Val Gly Asp Met Val Gln Leu Leu Cys Glu Ala Gln		
	180	185	190
	Arg Gly Ser Pro Pro Ile Leu Tyr Ser Phe Tyr Leu Asp Glu Lys Ile		
	195	200	205
	Val Gly Asn His Ser Ala Pro Cys Gly Gly Thr Thr Ser Leu Leu Phe		
25	210	215	220

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Pro Val Lys Ser Glu Gln Asp Ala Gly Asn Tyr Ser Cys Glu Ala Glu
225 230 235 240
Asn Ser Val Ser Arg Glu Arg Ser Glu Pro Lys Lys Leu Ser Leu Lys
245 250 255
5 Gly Ser Gln Val Leu Phe Thr Pro Ala Ser Asn Trp Leu Val Pro Trp
260 265 270
Leu Pro Ala Ser Leu Leu Gly Leu Met Val Ile Ala Ala Ala Leu Leu
275 280 285
Val Tyr Val Arg Ser Trp Arg Lys Ala Gly Pro Leu Pro Ser Gln Ile
10 290 295 300
Pro Pro Thr Ala Pro Gly Gly Glu Gln Cys Pro Leu Tyr Ala Asn Val
305 310 315 320
His His Gln Lys Gly Lys Asp Glu Gly Val Val Tyr Ser Val Val His
325 330 335
15 Arg Thr Ser Lys Arg Ser Glu Ala Arg Ser Ala Glu Phe Thr Val Gly
340 345 350
Arg Lys Asp Ser Ser Ile Ile Cys Ala Glu Val Arg Cys Leu Gln Pro
355 360 365
Ser Glu Val Ser Ser Thr Glu Val Asn Met Arg Ser Arg Thr Leu Gln
20 370 375 380
Glu Pro Leu Ser Asp Cys Glu Glu Val Leu Cys
385 390 395

<210> 122
25 <211> 550

275/346

<212> PRT

<213> Homo sapiens

<400> 122

5 Met Ala Phe Ser Lys Leu Leu Glu Gln Ala Gly Gly Val Gly Leu Phe
1 5 10 15
Gln Thr Leu Gln Val Leu Thr Phe Ile Leu Pro Cys Leu Met Ile Pro
20 25 30
Ser Gln Met Leu Leu Glu Asn Phe Ser Ala Ala Ile Pro Gly His Arg
10 35 40 45
Cys Trp Thr His Met Leu Asp Asn Gly Ser Ala Val Ser Thr Asn Met
50 55 60
Thr Pro Lys Ala Leu Leu Thr Ile Ser Ile Pro Pro Gly Pro Asn Gln
65 70 75 80
15 Gly Pro His Gln Cys Arg Arg Phe Arg Gln Pro Gln Trp Gln Leu Leu
85 90 95
Asp Pro Asn Ala Thr Ala Thr Ser Trp Ser Glu Ala Asp Thr Glu Pro
100 105 110
Cys Val Asp Gly Trp Val Tyr Asp Arg Ser Val Phe Thr Ser Thr Ile
20 115 120 125
Val Ala Lys Trp Asp Leu Val Cys Ser Ser Gln Gly Leu Lys Pro Leu
130 135 140
Ser Gln Ser Ile Phe Met Ser Gly Ile Leu Val Gly Ser Phe Ile Trp
145 150 155 160
25 Gly Leu Leu Ser Tyr Arg Phe Gly Arg Lys Pro Met Leu Ser Trp Cys

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	165	170	175
	Cys Leu Gln Leu Ala Val Ala Gly Thr Ser Thr Ile Phe Ala Pro Thr		
	180	185	190
	Phe Val Ile Tyr Cys Gly Leu Arg Phe Val Ala Ala Phe Gly Met Ala		
5	195	200	205
	Gly Ile Phe Leu Ser Ser Leu Thr Leu Met Val Glu Trp Thr Thr Thr		
	210	215	220
	Ser Arg Arg Ala Val Thr Met Thr Val Val Gly Cys Ala Phe Ser Ala		
	225	230	235 240
10	Gly Gln Ala Ala Leu Gly Gly Leu Ala Phe Ala Leu Arg Asp Trp Arg		
	245	250	255
	Thr Leu Gln Leu Ala Ala Ser Val Pro Phe Phe Ala Ile Ser Leu Ile		
	260	265	270
	Ser Trp Trp Leu Pro Glu Ser Ala Arg Trp Leu Ile Ile Lys Gly Lys		
15	275	280	285
	Pro Asp Gln Ala Leu Gln Glu Leu Arg Lys Val Ala Arg Ile Asn Gly		
	290	295	300
	His Lys Glu Ala Lys Asn Leu Thr Ile Glu Val Leu Met Ser Ser Val		
	305	310	315 320
20	Lys Glu Glu Val Ala Ser Ala Lys Glu Pro Arg Ser Val Leu Asp Leu		
	325	330	335
	Phe Cys Val Pro Val Leu Arg Trp Arg Ser Cys Ala Met Leu Val Val		
	340	345	350
	Asn Phe Ser Leu Leu Ile Ser Tyr Tyr Gly Leu Val Phe Asp Leu Gln		
25	355	360	365

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Ser Leu Gly Arg Asp Ile Phe Leu Leu Gln Ala Leu Phe Gly Ala Val
 370 375 380
 Asp Phe Leu Gly Arg Ala Thr Thr Ala Leu Leu Leu Ser Phe Leu Gly
 385 390 395 400
 5 Arg Arg Thr Ile Gln Ala Gly Ser Gln Ala Met Ala Gly Leu Ala Ile
 405 410 415
 Leu Ala Asn Met Leu Val Pro Gln Asp Leu Gln Thr Leu Arg Val Val
 420 425 430
 Phe Ala Val Leu Gly Lys Gly Cys Phe Gly Ile Ser Leu Thr Cys Leu
 10 435 440 445
 Thr Ile Tyr Lys Ala Glu Leu Phe Pro Thr Pro Val Arg Met Thr Ala
 450 455 460
 Asp Gly Ile Leu His Thr Val Gly Arg Leu Gly Ala Met Met Gly Pro
 465 470 475 480
 15 Leu Ile Leu Met Ser Arg Gln Ala Leu Pro Leu Leu Pro Pro Leu Leu
 485 490 495
 Tyr Gly Val Ile Ser Ile Ala Ser Ser Leu Val Val Leu Phe Phe Leu
 500 505 510
 Pro Glu Thr Gln Gly Leu Pro Leu Pro Asp Thr Ile Gln Asp Leu Glu
 20 515 520 525
 Ser Gln Lys Ser Thr Ala Ala Gln Gly Asn Arg Gln Glu Ala Val Thr
 530 535 540
 Val Glu Ser Thr Ser Leu
 545 550
 25

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<210> 123

<211> 218

<212> PRT

<213> Homo sapiens

5

<400> 123

Met Leu His Thr Leu Ala Leu Leu Ala Pro Leu Leu Gly Leu Gly Leu
1 5 10 15
Gly Leu Ala Leu Ser Gln Leu Ala Ala Gly Ala Thr Asp Cys Lys Phe
10 20 25 30
Leu Gly Pro Ala Glu His Leu Thr Phe Thr Pro Ala Ala Arg Ala Arg
35 40 45
Trp Leu Ala Pro Arg Val Arg Ala Pro Gly Leu Leu Asp Ser Leu Tyr
50 55 60
15 Gly Thr Val Arg Arg Phe Leu Ser Val Val Gln Leu Asn Pro Phe Pro
65 70 75 80
Ser Glu Leu Val Lys Ala Leu Leu Asn Glu Leu Ala Ser Val Lys Val
85 90 95
Asn Glu Val Val Arg Tyr Glu Ala Gly Tyr Val Val Cys Ala Val Ile
20 100 105 110
Ala Gly Leu Tyr Leu Leu Leu Val Pro Thr Ala Gly Leu Cys Phe Cys
115 120 125
Cys Cys Arg Cys His Arg Arg Cys Gly Gly Arg Val Lys Thr Glu His
130 135 140
25 Lys Ala Leu Ala Cys Glu Arg Ala Ala Leu Met Val Phe Leu Leu Leu

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145 150 155 160
Thr Thr Leu Leu Leu Leu Ile Gly Val Val Cys Ala Phe Val Thr Asn
165 170 175
Gln Arg Thr His Glu Gln Met Gly Pro Ser Ile Glu Ala Met Pro Glu
5 180 185 190
Thr Leu Leu Ser Leu Trp Gly Leu Val Ser Asp Val Pro Gln Val Ser
195 200 205
Thr Val Thr Pro His Pro His Val Pro Leu
210 215
10
<210> 124
<211> 596
<212> PRT
<213> Homo sapiens
15
<400> 124
Met Ala Ala Asn Ser Thr Ser Asp Leu His Thr Pro Gly Thr Gln Leu
1 5 10 15
Ser Val Ala Asp Ile Ile Val Ile Thr Val Tyr Phe Ala Leu Asn Val
20 20 25 30
Ala Val Gly Ile Trp Ser Ser Cys Arg Ala Ser Arg Asn Thr Val Asn
35 40 45
Gly Tyr Phe Leu Ala Gly Arg Asp Met Thr Trp Trp Pro Ile Gly Ala
50 55 60
25 Ser Leu Phe Ala Ser Ser Glu Gly Ser Gly Leu Phe Ile Gly Leu Ala

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	65		70		75		80
	Gly Ser Gly Ala Ala Gly Gly Leu Ala Val Ala Gly Phe Glu Trp Asn						
		85		90		95	
	Ala Thr Tyr Val Leu Leu Ala Leu Ala Trp Val Phe Val Pro Ile Tyr						
5		100		105		110	
	Ile Ser Ser Glu Ile Val Thr Leu Pro Glu Tyr Ile Gln Lys Arg Tyr						
		115		120		125	
	Gly Gly Gln Arg Ile Arg Met Tyr Leu Ser Val Leu Ser Leu Leu Leu						
		130		135		140	
10	Ser Val Phe Thr Lys Ile Ser Leu Asp Leu Tyr Ala Gly Ala Leu Phe						
		145		150		155	160
	Val His Ile Cys Leu Gly Trp Asn Phe Tyr Leu Ser Thr Ile Leu Thr						
		165		170		175	
	Leu Gly Ile Thr Ala Leu Tyr Thr Ile Ala Gly Gly Leu Ala Ala Val						
15		180		185		190	
	Ile Tyr Thr Asp Ala Leu Gln Thr Leu Ile Met Val Val Gly Ala Val						
		195		200		205	
	Ile Leu Thr Ile Lys Ala Phe Asp Gln Ile Gly Gly Tyr Gly Gln Leu						
		210		215		220	
20	Glu Ala Ala Tyr Ala Gln Ala Ile Pro Ser Arg Thr Ile Ala Asn Thr						
		225		230		235	240
	Thr Cys His Leu Pro Arg Thr Asp Ala Met His Met Phe Arg Asp Pro						
		245		250		255	
	His Thr Gly Asp Leu Pro Trp Thr Gly Met Thr Phe Gly Leu Thr Ile						
25		260		265		270	

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Met Ala Thr Trp Tyr Trp Cys Thr Asp Gln Val Ile Val Gln Arg Ser
275 280 285

Leu Ser Ala Arg Asp Leu Asn His Ala Lys Ala Gly Ser Ile Leu Ala
290 295 300

5 Ser Tyr Leu Lys Met Leu Pro Met Gly Leu Ile Ile Met Pro Gly Met
305 310 315 320

Ile Ser Arg Ala Leu Phe Pro Asp Asp Val Gly Cys Val Val Pro Ser
325 330 335

Glu Cys Leu Arg Ala Cys Gly Ala Glu Val Gly Cys Ser Asn Ile Ala
10 340 345 350

Tyr Pro Lys Leu Val Met Glu Leu Met Pro Ile Gly Leu Arg Gly Leu
355 360 365

Met Ile Ala Val Met Leu Ala Ala Leu Met Ser Ser Leu Thr Ser Ile
370 375 380

15 Phe Asn Ser Ser Ser Thr Leu Phe Thr Met Asp Ile Trp Arg Arg Leu
385 390 395 400

Arg Pro Arg Ser Gly Glu Arg Glu Leu Leu Leu Val Gly Arg Leu Val
405 410 415

Ile Val Ala Leu Ile Gly Val Ser Val Ala Trp Ile Pro Val Leu Gln
20 420 425 430

Asp Ser Asn Ser Gly Gln Leu Phe Ile Tyr Met Gln Ser Val Thr Ser
435 440 445

Ser Leu Ala Pro Pro Val Thr Ala Val Phe Val Leu Gly Val Phe Trp
450 455 460

25 Arg Arg Ala Asn Glu Gln Gly Ala Phe Trp Gly Leu Ile Ala Gly Leu

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465 470 475 480
Val Val Gly Ala Thr Arg Leu Val Leu Glu Phe Leu Asn Pro Ala Pro
 485 490 495
Pro Cys Gly Glu Pro Asp Thr Arg Pro Ala Val Leu Gly Ser Ile His
5 500 505 510
Tyr Leu His Phe Ala Val Ala Leu Phe Ala Leu Ser Gly Ala Val Val
 515 520 525
Val Ala Gly Ser Leu Leu Thr Pro Pro Pro Gln Ser Val Gln Ile Glu
 530 535 540
10 Asn Leu Thr Trp Trp Thr Leu Ala Gln Asp Val Pro Leu Gly Thr Lys
 545 550 555 560
Ala Gly Asp Gly Gln Thr Pro Gln Lys His Ala Phe Trp Ala Arg Val
 565 570 575
Cys Gly Phe Asn Ala Ile Leu Leu Met Cys Val Asn Ile Phe Phe Tyr
15 580 585 590
Ala Tyr Phe Ala
 595

<210> 125
20 <211> 467
<212> PRT
<213> Homo sapiens

<400> 125
25 Met Trp Arg Cys Pro Leu Gly Leu Leu Leu Leu Leu Pro Leu Ala Gly

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	1	5	10	15
	His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala			
	20	25	30	
	Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys			
5	35	40	45	
	Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu			
	50	55	60	
	Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr			
	65	70	75	80
10	Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro			
	85	90	95	
	Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr			
	100	105	110	
	Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln			
15	115	120	125	
	Glu Asn Arg Gln Trp Gln Cys Asp Gln Glu Pro Cys Leu Val Asp Pro			
	130	135	140	
	Asp Met Ile Lys Ala Ile Asn Gln Gly Asn Tyr Gly Trp Gln Ala Gly			
	145	150	155	160
20	Asn His Ser Ala Phe Trp Gly Met Thr Leu Asp Glu Gly Ile Arg Tyr			
	165	170	175	
	Arg Leu Gly Thr Ile Arg Pro Ser Ser Ser Val Met Asn Met His Glu			
	180	185	190	
	Ile Tyr Thr Val Leu Asn Pro Gly Glu Val Leu Pro Thr Ala Phe Glu			
25	195	200	205	

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Ala Ser Glu Lys Trp Pro Asn Leu Ile His Glu Pro Leu Asp Gln Gly
 210 215 220
 Asn Cys Ala Gly Ser Trp Ala Phe Ser Thr Ala Ala Val Ala Ser Asp
 225 230 235 240
 5 Arg Val Ser Ile His Ser Leu Gly His Met Thr Pro Val Leu Ser Pro
 245 250 255
 Gln Asn Leu Leu Ser Cys Asp Thr His Gln Gln Gln Gly Cys Arg Gly
 260 265 270
 Gly Arg Leu Asp Gly Ala Trp Trp Phe Leu Arg Arg Arg Gly Val Val
 10 275 280 285
 Ser Asp His Cys Tyr Pro Phe Ser Gly Arg Glu Arg Asp Glu Ala Gly
 290 295 300
 Pro Ala Pro Pro Cys Met Met His Ser Arg Ala Met Gly Arg Gly Lys
 305 310 315 320
 15 Arg Gln Ala Thr Ala His Cys Pro Asn Ser Tyr Val Asn Asn Asn Asp
 325 330 335
 Ile Tyr Gln Val Thr Pro Val Tyr Arg Leu Gly Ser Asn Asp Lys Glu
 340 345 350
 Ile Met Lys Glu Leu Met Glu Asn Gly Pro Val Gln Ala Leu Met Glu
 20 355 360 365
 Val His Glu Asp Phe Phe Leu Tyr Lys Gly Gly Ile Tyr Ser His Thr
 370 375 380
 Pro Val Ser Leu Gly Arg Pro Glu Arg Tyr Arg Arg His Gly Thr His
 385 390 395 400
 25 Ser Val Lys Ile Thr Gly Trp Gly Glu Glu Thr Leu Pro Asp Gly Arg

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405 410 415
Thr Leu Lys Tyr Trp Thr Ala Ala Asn Ser Trp Gly Pro Ala Trp Gly
420 425 430
Glu Arg Gly His Phe Arg Ile Val Arg Gly Val Asn Glu Cys Asp Ile
5 435 440 445
Glu Ser Phe Val Leu Gly Val Trp Gly Arg Val Gly Met Glu Asp Met
450 455 460
Gly His His
465
10
<210> 126
<211> 476
<212> PRT
<213> Homo sapiens
15
<400> 126
Met Ala Gly Ser Asp Thr Ala Pro Phe Leu Ser Gln Ala Asp Asp Pro
1 5 10 15
Asp Asp Gly Pro Val Pro Gly Thr Pro Gly Leu Pro Gly Ser Thr Gly
20 20 25 30
Asn Pro Lys Ser Glu Glu Pro Glu Val Pro Asp Gln Glu Gly Leu Gln
35 40 45
Arg Ile Thr Gly Leu Ser Pro Gly Arg Ser Ala Leu Ile Val Ala Val
50 55 60
25 Leu Cys Tyr Ile Asn Leu Leu Asn Tyr Met Asp Arg Phe Thr Val Ala

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	65	70	75	80
	Gly Val Leu Pro Asp Ile Glu Gln Phe Phe Asn Ile Gly Asp Ser Ser			
	85	90	95	
	Ser Gly Leu Ile Gln Thr Val Phe Ile Ser Ser Tyr Met Val Leu Ala			
5	100	105	110	
	Pro Val Phe Gly Tyr Leu Gly Asp Arg Tyr Asn Arg Lys Tyr Leu Met			
	115	120	125	
	Cys Gly Gly Ile Ala Phe Trp Ser Leu Val Thr Leu Gly Ser Ser Phe			
	130	135	140	
10	Ile Pro Gly Glu His Phe Trp Leu Leu Leu Leu Thr Arg Gly Leu Val			
	145	150	155	160
	Gly Val Gly Glu Ala Ser Tyr Ser Thr Ile Ala Pro Thr Leu Ile Ala			
	165	170	175	
	Asp Leu Phe Val Ala Asp Gln Arg Ser Arg Met Leu Ser Ile Phe Tyr			
15	180	185	190	
	Phe Ala Ile Pro Val Gly Ser Gly Leu Gly Tyr Ile Ala Gly Ser Lys			
	195	200	205	
	Val Lys Asp Met Ala Gly Asp Trp His Trp Ala Leu Arg Val Thr Pro			
	210	215	220	
20	Gly Leu Gly Val Val Ala Val Leu Leu Leu Phe Leu Val Val Arg Glu			
	225	230	235	240
	Pro Pro Arg Gly Ala Val Glu Arg His Ser Asp Leu Pro Pro Leu Asn			
	245	250	255	
	Pro Thr Ser Trp Trp Ala Asp Leu Arg Ala Leu Ala Arg Asn Leu Ile			
25	260	265	270	

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Phe Gly Leu Ile Thr Cys Leu Thr Gly Val Leu Gly Val Gly Leu Gly
 275 280 285
 Val Glu Ile Ser Arg Arg Leu Arg His Ser Asn Pro Arg Ala Asp Pro
 290 295 300
 5 Leu Val Cys Ala Thr Gly Leu Leu Gly Ser Ala Pro Phe Leu Phe Leu
 305 310 315 320
 Ser Leu Ala Cys Ala Arg Gly Ser Ile Val Ala Thr Tyr Ile Phe Ile
 325 330 335
 Phe Ile Gly Glu Thr Leu Leu Ser Met Asn Trp Ala Ile Val Ala Asp
 10 340 345 350
 Ile Leu Leu Tyr Val Val Ile Pro Thr Arg Arg Ser Thr Ala Glu Ala
 355 360 365
 Phe Gln Ile Val Leu Ser His Leu Leu Gly Asp Ala Gly Ser Pro Tyr
 370 375 380
 15 Leu Ile Gly Leu Ile Ser Asp Arg Leu Arg Arg Asn Trp Pro Pro Ser
 385 390 395 400
 Phe Leu Ser Glu Phe Arg Ala Leu Gln Phe Ser Leu Met Leu Cys Ala
 405 410 415
 Phe Val Gly Ala Leu Gly Gly Ala Ala Phe Leu Gly Thr Ala Ile Phe
 20 420 425 430
 Ile Glu Ala Asp Arg Arg Arg Ala Gln Leu His Val Gln Gly Leu Leu
 435 440 445
 His Glu Ala Gly Ser Thr Asp Asp Arg Ile Val Val Pro Gln Arg Gly
 450 455 460
 25 Arg Ser Thr Arg Val Pro Val Ala Ser Val Leu Ile

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465

470

475

<210> 127

<211> 449

5 <212> PRT

<213> Homo sapiens

<400> 127

Met Ser Asp Ile Arg His Ser Leu Leu Arg Arg Asp Ala Leu Ser Ala

10 1 5 10 15

Ala Lys Glu Val Leu Tyr His Leu Asp Ile Tyr Phe Ser Ser Gln Leu

20 25 30

Gln Ser Ala Pro Leu Pro Ile Val Asp Lys Gly Pro Val Glu Leu Leu

35 40 45

15 Glu Glu Phe Val Phe Gln Val Pro Lys Glu Arg Ser Ala Gln Pro Lys

50 55 60

Arg Leu Asn Ser Leu Gln Glu Leu Gln Leu Leu Glu Ile Met Cys Asn

65 70 75 80

Tyr Phe Gln Glu Gln Thr Lys Asp Ser Val Arg Gln Ile Ile Phe Ser

20 85 90 95

Ser Leu Phe Ser Pro Gln Gly Asn Lys Ala Asp Asp Ser Arg Met Ser

100 105 110

Leu Leu Gly Lys Leu Val Ser Met Ala Val Ala Val Cys Arg Ile Pro

115 120 125

25 Val Leu Glu Cys Ala Ala Ser Trp Leu Gln Arg Thr Pro Val Val Tyr

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	130	135	140	
	Cys Val Arg Leu Ala Lys Ala Leu Val Asp Asp Tyr Cys Cys Leu Val			
	145	150	155	160
	Pro Gly Ser Ile Gln Thr Leu Lys Gln Ile Phe Ser Ala Ser Pro Arg			
5	165	170	175	
	Phe Cys Cys Gln Phe Ile Thr Ser Val Thr Ala Leu Tyr Asp Leu Ser			
	180	185	190	
	Ser Asp Asp Leu Ile Pro Pro Met Asp Leu Leu Glu Met Ile Val Thr			
	195	200	205	
10	Trp Ile Phe Glu Asp Pro Arg Leu Ile Leu Ile Thr Phe Leu Asn Thr			
	210	215	220	
	Pro Ile Ala Ala Asn Leu Pro Ile Gly Phe Leu Glu Leu Thr Pro Leu			
	225	230	235	240
	Val Gly Leu Ile Arg Trp Cys Val Lys Ala Pro Leu Ala Tyr Lys Arg			
15	245	250	255	
	Lys Lys Lys Pro Pro Leu Ser Asn Gly His Val Ser Asn Lys Val Thr			
	260	265	270	
	Lys Asp Pro Gly Val Gly Met Asp Arg Asp Ser His Leu Leu Tyr Ser			
	275	280	285	
20	Lys Leu His Leu Ser Val Leu Gln Val Leu Met Thr Leu Gln Leu His			
	290	295	300	
	Leu Thr Glu Lys Asn Leu Tyr Gly Arg Leu Gly Leu Ile Leu Phe Asp			
	305	310	315	320
	His Met Val Pro Leu Val Glu Glu Ile Asn Arg Leu Ala Asp Glu Leu			
25	325	330	335	

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Asn Pro Leu Asn Ala Ser Gln Glu Ile Glu Leu Ser Leu Asp Arg Leu
340 345 350

Ala Gln Ala Leu Gln Val Ala Met Ala Ser Gly Ala Leu Leu Cys Thr
355 360 365

5 Arg Asp Asp Leu Arg Thr Leu Cys Ser Arg Leu Pro His Asn Asn Leu
370 375 380

Leu Gln Leu Val Ile Ser Gly Pro Val Gln Gln Ser Pro His Ala Ala
385 390 395 400

Leu Pro Pro Gly Phe Tyr Pro His Ile His Thr Pro Pro Leu Gly Tyr
10 405 410 415

Gly Ala Val Pro Ala His Pro Ala Ala His Pro Ala Leu Pro Thr His
420 425 430

Pro Gly His Thr Phe Ile Ser Gly Val Thr Phe Pro Phe Arg Pro Ile
435 440 445

15 Arg

<210> 128

<211> 105

20 <212> PRT

<213> Homo sapiens

<400> 128

Met Arg Arg Ile Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Phe
25 1 5 10 15

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Leu Leu Leu Leu Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser
      20              25              30
Leu Cys Phe Asn Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro
      35              40              45
5  Trp Cys Glu Ala Gln Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr
      50              55              60
Asn Ser Asp Asn Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys
      65              70              75              80
Val Asn Ala Thr Ser Thr Trp Gly Glu Asn Pro Asn Ala Gly Arg Ser
10              85              90              95
Gly Ala Arg Pro Gln Asp Ala Pro Leu
      100              105

<210> 129
15 <211> 81
    <212> PRT
    <213> Homo sapiens

<400> 129
20 Met Ser Pro Asp Val Arg Phe Leu Leu Leu Leu Leu Leu Pro Leu
    1              5              10              15
Arg Arg Pro Val Pro Val Ala Ala Gly Pro Gly Asp Thr Arg Pro Ala
      20              25              30
Leu Leu Ser Phe Glu Ala Pro Val Phe Val Pro Thr Leu Thr Pro Gly
25              35              40              45

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Cys Leu Gln Gln Pro Arg Gly Arg Asn Gly Ala Ser Pro Arg Gly Leu
 50 55 60
 Leu Pro Gln Pro Leu Asp Gly Thr Ala Ala Ser Pro Val Cys His His
 65 70 75 80
 5 Val

 <210> 130
 <211> 552
 10 <212> PRT
 <213> Homo sapiens

 <400> 130
 Met Arg Arg Leu Thr Arg Arg Leu Val Leu Pro Val Phe Gly Val Leu
 15 1 5 10 15
 Trp Ile Thr Val Leu Leu Phe Phe Trp Val Thr Lys Arg Lys Leu Glu
 20 25 30
 Val Pro Thr Gly Pro Glu Val Gln Thr Pro Lys Pro Ser Asp Ala Asp
 35 40 45
 20 Trp Asp Asp Leu Trp Asp Gln Phe Asp Glu Arg Arg Tyr Leu Asn Ala
 50 55 60
 Lys Lys Trp Arg Val Gly Asp Asp Pro Tyr Lys Leu Tyr Ala Phe Asn
 65 70 75 80
 Gln Arg Glu Ser Glu Arg Ile Ser Ser Asn Arg Ala Ile Pro Asp Thr
 25 85 90 95

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	Arg His Leu Arg Cys Thr Leu Leu Val Tyr Cys Thr Asp Leu Pro Pro	
	100	105 110
	Thr Ser Ile Ile Ile Thr Phe His Asn Glu Ala Arg Ser Thr Leu Leu	
	115	120 125
5	Arg Thr Ile Arg Ser Val Leu Asn Arg Thr Pro Thr His Leu Ile Arg	
	130	135 140
	Glu Ile Ile Leu Val Asp Asp Phe Ser Asn Asp Pro Asp Asp Cys Lys	
	145	150 155 160
	Gln Leu Ile Lys Leu Pro Lys Val Lys Cys Leu Arg Asn Asn Glu Arg	
10	165	170 175
	Gln Gly Leu Val Arg Ser Arg Ile Arg Gly Ala Asp Ile Ala Gln Gly	
	180	185 190
	Thr Thr Leu Thr Phe Leu Asp Ser His Cys Glu Val Asn Arg Asp Trp	
	195	200 205
15	Leu Gln Pro Leu Leu His Arg Val Lys Glu Asp Tyr Thr Arg Val Val	
	210	215 220
	Cys Pro Val Ile Asp Ile Ile Asn Leu Asp Thr Phe Thr Tyr Ile Glu	
	225	230 235 240
	Ser Ala Ser Glu Leu Arg Gly Gly Phe Asp Trp Ser Leu His Phe Gln	
20	245	250 255
	Trp Glu Gln Leu Ser Pro Glu Gln Lys Ala Arg Arg Leu Asp Pro Thr	
	260	265 270
	Glu Pro Ile Arg Thr Pro Ile Ile Ala Gly Gly Leu Phe Val Ile Asp	
	275	280 285
25	Lys Ala Trp Phe Asp Tyr Leu Gly Lys Tyr Asp Met Asp Met Asp Ile	

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	290	295	300	
	Trp Gly Gly Glu Asn Phe Glu Ile Ser Phe Arg Val Trp Met Cys Gly			
	305	310	315	320
	Gly Ser Leu Glu Ile Val Pro Cys Ser Arg Val Gly His Val Phe Arg			
5	325	330	335	
	Lys Lys His Pro Tyr Val Phe Pro Asp Gly Asn Ala Asn Thr Tyr Ile			
	340	345	350	
	Lys Asn Thr Lys Arg Thr Ala Glu Val Trp Met Asp Glu Tyr Lys Gln			
	355	360	365	
10	Tyr Tyr Tyr Ala Ala Arg Pro Phe Ala Leu Glu Arg Pro Phe Gly Asn			
	370	375	380	
	Val Glu Ser Arg Leu Asp Leu Arg Lys Asn Leu Arg Cys Gln Ser Phe			
	385	390	395	400
	Lys Trp Tyr Leu Glu Asn Ile Tyr Pro Glu Leu Ser Ile Pro Lys Glu			
15	405	410	415	
	Ser Ser Ile Gln Lys Gly Asn Ile Arg Gln Arg Gln Lys Cys Leu Glu			
	420	425	430	
	Ser Gln Arg Gln Asn Asn Gln Glu Thr Pro Asn Leu Lys Leu Ser Pro			
	435	440	445	
20	Cys Ala Lys Val Lys Gly Glu Asp Ala Lys Ser Gln Val Trp Ala Phe			
	450	455	460	
	Thr Tyr Thr Gln Gln Ile Leu Gln Glu Glu Leu Cys Leu Ser Val Ile			
	465	470	475	480
	Thr Leu Phe Pro Gly Ala Pro Val Val Leu Val Leu Cys Lys Asn Gly			
25	485	490	495	

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Asp Asp Arg Gln Gln Trp Thr Lys Thr Gly Ser His Ile Glu His Ile
 500 505 510
 Ala Ser His Leu Cys Leu Asp Thr Asp Met Phe Gly Asp Gly Thr Glu
 515 520 525
 5 Asn Gly Lys Glu Ile Val Val Asn Pro Cys Glu Ser Ser Leu Met Ser
 530 535 540
 Gln His Trp Asp Met Val Ser Ser
 545 550
 10 <210> 131
 <211> 1188
 <212> DNA
 <213> Homo sapiens
 15 <400> 131
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 ccttcattta aggaaaacca gactctgtcc atgggagcag caacagtgc gagccgtggc 120
 cagtacagct gctctgggca ggtgatgtat attccacaga cattcacaca aacttcagag 180
 actgccatgg ttcaagtcca agagctgttt ccacctcctg tgctgagtgc catcccctct 240
 20 cctgagcccc gagagggtag cctggtgacc ctgagatgtc agacaaagct gcaccccctg 300
 aggtcagcct tgaggctcct tttctccttc cacaaggacg gccacacctt gcaggacagg 360
 ggccctcacc cagaactctg catcccggga gccaaaggagg gagactctgg gctttactgg 420
 tgtgaggtgg cccctgaggg tggccaggtc cagaagcaga gccccagct ggaggtcaga 480
 gtgcaggctc ctgtatcccg tcctgtgtc actctgcacc acgggcctgc tgaccctgct 540
 25 gtgggggaca tgggtgcagct cctctgtgag gcacagaggg gctcccctcc gatcctgtat 600

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tccttctacc ttgatgagaa gattgtgggg aaccactcag ctccctgtgg tggaaccacc 660
tccctcctct tcccagtga gtcagaacag gatgctggga actactcctg cgaggctgag 720
aacagtgtct ccagagagag gagtgagccc aagaagctgt ctctgaaggg ttctcaagtc 780
ttgttcactc ccgccagcaa ctggctgggt ccttggttc ctgcgagcct gcttggcctg 840
5 atggttattg ctgctgcaact tctggtttat gtgagatcct ggagaaaagc tgggcccctt 900
ccatcccaga taccacccac agctccaggt ggagagcagt gccactata tgccaacgtg 960
catcaccaga aagggaaga tgaagtggt gtctactctg tgggtcatag aacctcaaag 1020
aggagtgaag ccaggtctgc tgagttcacc gtggggagaa aggacagttc tatcatctgt 1080
gcggaggtga gatgcctgca gccagtgag gtttcatcca cggaggtgaa tatgagaagc 1140
10 aggactctcc aagaaccct tagcgactgt gaggaggttc tctgctag 1188

<210> 132

<211> 1653

<212> DNA

15 <213> Homo sapiens

<400> 132

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gtgctcacct tcacctccc ctgcctcatg atacctccc agatgctcct ggagaacttc 120
20 tcagccgcca tcccaggcca ccgatgctgg acacacatgc tggacaatgg ctctgcggtt 180
tccacaaaca tgaccccaa ggcccttctg accatctcca tcccgccagg cccaaccag 240
gggccccacc agtgccgccc cttccgccag ccacagtggc agctcttgga cccaatgcc 300
acggccacca gctggagcga agctgacacg gagccgtgtg tggacggctg ggtctatgac 360
cgcagcgtct tcacctccac catcgtggcc aagtgggacc tgggtgtgag ctcccagggc 420
25 ttgaagcccc taagccagtc catcttcatg tccgggatcc tgggtgggtc ctttatctgg 480

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ggcctcctct cctaccggtt tgggaggaag cccatgctga gctgggtgctg cctgcagttg 540
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ttcgtggccg cttttgggat ggccggcatc tttctgagtt cactgacact gatgggtggag 660
tggaccacga ccagcaggag ggcggtcacc atgacgggtg tgggatgtgc cttcagcgca 720
5 ggcagggcgg cgctgggcgg cctggccttt gccctgcggg actggaggac tctccagctg 780
gcagcatcag tgcccttctt tgccatctcc ctgatatact ggtgggtgcc agaatacgcc 840
cggtggtgta ttattaaggg caaaccagac caagcacttc aggagctcag aaagggtggcc 900
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10 gtgctccgct ggaggagctg cgccatgctg gtggtgaatt tctctctatt gatctoctac 1080
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ttcggggccg tggacttcct gggccgggcc accactgccc tcttgctcag tttccttggc 1200
cgccgcacca tccaggcggg ttcccaggcc atggccggcc tcgccattct agccaacatg 1260
ctggtgccgc aagatttgca gacctgctg gtggtctttg ctgtgctggg aaagggatgt 1320
15 tttgggataa gcctaacctg cctcaccatc tacaaggctg aactctttcc aacgccagt 1380
cggatgacag cagatggcat tctgcataca gtgggccggc tgggggctat gatgggtccc 1440
ctgatcctga tgagccgcca agccctgccc ctgctgctc ctctcctcta tggcgttata 1500
tccattgctt ccagcctggg tgtgctgttc ttcctcccg agaccaggg acttccgctc 1560
cctgacacta tccaggacct ggagagccag aaatcaacag cagcccaggg caaccggcaa 1620
20 gaggccgtca ctgtggaag tacctcgtc tag 1653

<210> 133

<211> 657

<212> DNA

25 <213> Homo sapiens

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<400> 133

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agtcagctgg ctgcaggggc cacagactgc aagttccttg gcccggcaga gcacctgaca 120
5 ttcaccccag cagccagggc ccggtggctg gccctcgag ttcgtgcgcc aggactcctg 180
gactccctct atggcacctg gcgccgttc ctctcgggtg tgcagctcaa tcctttccct 240
tcagagttgg taaaggccct actgaatgag ctggcctccg tgaagtgaa tgaggtgggtg 300
cggtagcagg cgggctacgt ggtatgcgt gtgatgcgg gcctctacct gctgctgggtg 360
cccactgccg ggctttgctt ctgctgctgc cgtgccacc ggcgctgcgg gggacgagtg 420
10 aagacagagc acaaggcgt ggctgtgag cgcgcggccc tcatggtctt cctgctgctg 480
accacccctt tgctgctgat tgggtgtggtc tgtgccttg tcaccaacca gcgcacgcat 540
gaacagatgg gcccagcat cgaggccatg cctgagacc tgctcagcct ctggggcctg 600
gtctctgatg tcccccaagt gagcactgtt acccctcacc ctcatgtgcc cctgtga 657

15 <210> 134

<211> 1791

<212> DNA

<213> Homo sapiens

20 <400> 134

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atcatcgtca tcaactgtgta ttttgctctg aatgtggccg tgggcatatg gtctcttctg 120
cgggccagta ggaacacggt gaatggctac ttcctggcag gccgggacat gacgtgggtg 180
ccgattggag cctccctctt cgccagcagc gagggctctg gcctcttcat tggactggcg 240
25 ggctcaggcg cggcaggagg tctggccgtg gcaggcttcg agtggaatgc cagtacgtg 300

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ctgctggcac tggcatgggt gttcgtgcc atctacatct cctcagagat cgtcacctta 360
cctgagtaca ttcagaagcg ctacgggggc cagcggatcc gcatgtacct gtctgtcctg 420
tcctgtctac tgtctgtctt caccaagata tcgctggacc tgtaacgggg ggctctgttt 480
gtgcacatct gcctgggctg gaactttctac ctctccacca tcctcacgct cggcatcaca 540
5 gccctgtaca ccatcgagcgg gggcctggct gctgtaatct acacggagcg cctgcagacg 600
ctcatcatgg tgggtggggc tgtcatcctg acaatcaaag cttttgacca gatcggtggt 660
tacgggcagc tggaggcagc ctaogcccag gccattccct ccaggaccat tgccaacacc 720
acctgccacc tgccacgtac agacgccatg cacatgtttc gagaccccca cacaggggac 780
ctgccgtgga ccgggatgac ctttggcctg accatcatgg ccacctggta ctggtgcacc 840
10 gaccaggtca tcgtgcagcg atcactgtca gcccgggacc tgaaccatgc caaggcgggc 900
tccatcctgg ccagctacct caagatgctc cccatgggcc tgatcataat gccgggcatg 960
atcagccgcg cattgttccc agatgatgtg ggctgcgtgg tgccgtccga gtgcctgcgg 1020
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atgcccatcg gtctgcgggg gctgatgatc gcagtgatgc tggcggcgct catgtcgtcg 1140
15 ctgacctcca tcttcaacag cagcagcacc ctcttacta tggacatctg gaggcggtg 1200
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ggcgtcttct ggcgacgtgc caacgagcag ggggccttct ggggcctgat agcagggctg 1440
20 gtggtggggg ccacgaggct ggtcctggaa ttctgaacc cagccccacc gtgcggagag 1500
ccagacacgc ggccagccgt cctggggagc atccactacc tgcacttcgc tgtcgccctc 1560
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gtccagattg agaaccttac ctggtggacc ctggctcagg atgtgccctt gggaactaaa 1680
gcaggtgatg gccaaacacc ccagaaacac gccttctggg cccgtgtctg tggcttcaat 1740
25 gccatcctcc tcatgtgtgt caacatatc ttttatgcct acttcgctg a 1791

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<210> 135

<211> 1404

<212> DNA

5 <213> Homo sapiens

<400> 135

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10 cgggacgcgg gaggccgta ctgccaggag caggacctgt gctgccgcgg ccgtgccgac 180
gactgtgccc tgcctacct gggcgccatc tgttactgtg acctcttctg caaccgcacg 240
gtctccgact gctgccctga cttctgggac ttctgcctcg gcgtgccacc cccttttccc 300
ccgatccaag gatgtatgca tggaggctcg atctatccag tcttgggaac gtactgggac 360
aactgtaacc gttgcacctg ccaggagaac aggcagtggc agtgtgacca agaaccatgc 420
15 ctggtggatc cagacatgat caaagccatc aaccagggca actatggctg gcaggctggg 480
aaccacagcg ccttctgggg catgaccctg gatgagggca ttcgctaccg cctgggcacc 540
atccgcccat ctctctcggg catgaacatg catgaaattt atacagtgtg gaaccaggg 600
gagggtgctt ccacagcctt cgaggcctct gagaagtggc ccaacctgat tcatgagcct 660
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20 cgtgtctcaa tccattctct gggacacatg acgcctgtcc tgcgccccca gaacctgtctg 780
tcttgtgaca cccaccagca gcagggtgc cgcggtgggc gtctcgatgg tgcctggtgg 840
ttctgcgtc gccgaggggt ggtgtctgac cactgctacc ctttctcggg ccgtgaacga 900
gacgaggctg gccctgcgcc cccctgtatg atgcacagcc gagccatggg tcggggcaag 960
cgccaggcca ctgcccactg cccaacagc tatgttaata acaatgacat ctaccaggtc 1020
25 actcctgtct accgcctcgg ctccaacgac aaggagatca tgaaggagct gatggagaat 1080

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tacagccaca cgccagttag ccttgggagg ccagagagat accgccggca tgggaccac 1200
tcagtcaaga tcacaggatg gggagaggag acgctgccag atggaaggac gctcaaatac 1260
tggactgcgg ccaactcctg gggcccagcc tggggcgaga ggggccactt ccgcatcgtg 1320
5 cgcgcggtca atgagtgcga catcgagagc ttctgtgctgg gcgtctgggg ccgctggggc 1380
atggaggaca tgggtcatca ctga 1404

<210> 136

<211> 1431

10 <212> DNA

<213> Homo sapiens

<400> 136

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15 gtgcctggca ccccggggtt gccagggtcc acggggaacc cgaagtccga ggagcccgag 120
gtcccggacc aggaggggct gcagcgcac accggcctgt ctcccgccg ttccggtctc 180
atagtggcgg tgctgtgcta catcaatctc ctgaactaca tggaccgctt caccgtggct 240
ggcgtccttc ccgacatcga gcagttcttc aacatcgggg acagtagctc tgggctcatc 300
cagaccgtgt tcatctccag ttacatggtg ttggcacctg tgtttggtta cctgggtgac 360
20 aggtacaatc ggaagtatct catgtgcggg ggcatcgctt tctggtcctt ggtgacactg 420
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gccgaccagc ggagccggat gctcagcatc ttctactttg ccattccggt gggcagtggg 600
ctgggttaca ttgcaggctc caaagtgaag gatatggctg gagactggca ctgggctctg 660
25 agggtgacac cgggtctagg agtgggtggc gttctgctgc tggttcctgg agtgccggag 720

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ccgccaaggg gagccgtgga gcgccactca gatttgccac ccctgaaccc cacctcgtgg 780
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cgggctgata ccctgggtctg tgccactggc ctctgggct ctgcaccctt cctcttctctg 960
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cagctgcacg tgcagggcct gctgcacgaa gcagggcca cagacgaccg gattgtggtg 1380
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<210> 137

15 <211> 1350

<212> DNA

<213> Homo sapiens

<400> 137

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gacaagggcc ccgtggagct gctggaggag ttcgtgttcc aggtgcccaa ggagcgcagc 180
gcgcagccca agagactgaa ttcccttcag gagcttcaac ttcttgaaat catgtgcaat 240
tatttccagg agcaaaccga ggactctgtt cggcagatta ttttttcata ctttttcagc 300
25 cctcaaggga acaaagccga tgacagccgg atgagcttgt tgggaaaact ggtctccatg 360

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gcggtggctg tgtgtcgaat cccggtgttg gagtgtgctg cctcctggct tcagcggacg 420
cccgtggttt actgtgtgag gttagccaag gcccttgtag atgactactg ctgtttgggtg 480
ccgggatcca ttcagacgct gaagcagata ttcagtgcc a gcccagatt ctgctgccag 540
ttcatcacct ccgttacgc gctctatgac ctgtcatcag atgacctcat tccacctatg 600
5 gacttgcttg aaatgattgt cacctggatt tttgaggacc caaggttgat tctcatcact 660
tttttaaata ctccgattgc ggccaatctg ccaataggat tcttagagct caccgccgctc 720
gttggtattga tccgctgggtg cgtgaaggca cccctggctt ataaaaggaa aaagaagccc 780
cccttatcca atggccatgt cagcaacaag gtcacaaagg acccgggctg ggggatggac 840
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10 ctgcagctgc acctgaccga gaagaatctg tatgggcgcc tggggctgat cctcttcgac 960
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15 ctcccccccg ggttctaccc ccacatccac acgccccgc tgggctacgg ggctgtcccg 1260
gccacccccg ccgccaccc cgccctgcc acgcaccccg gccacacctt catctccggc 1320
gtgacctttc ccttcaggcc catccgctag 1350

<210> 138

20 <211> 318

<212> DNA

<213> Homo sapiens

<400> 138

25 atgcgaagaa tatccctgac ttctagccct gtgcgccttc tttgtttct gctgttgcta 60

304/346

ctaatagcct tggagatcat ggttggtggt cactctcttt gcttcaactt cactataaaa 120
tcattgtcca gacctggaca gccctggtgt gaagcgagg tcttcttgaa taaaaatctt 180
ttccttcagt acaacagtga caacaacatg gtcaaacctc tgggcctcct gggaagaag 240
gtaaatgccca ccagcacttg gggagaaaac ccaaacgctg ggagaagtgg ggcgagacct 300
5 caggatgctc ctttgtga 318

<210> 139

<211> 246

<212> DNA

10 <213> Homo sapiens

<400> 139

atgagccctg atgtgcgctt tctgctcctg ctctgctcc tgccccttcg gaggcctgtg 60
ccagtggcag ctgggcccg agacaccagg ccggcactgc tctctttcga ggcacccgtg 120
15 tttgtgccga cgctgactcc cggttgtctg cagcagccac gtggccgaaa tggagcctct 180
ccacgggggc tccttcccca gccctggat ggcacagcag cctctcctgt ctgtcaccac 240
gtgtga 246

<210> 140

20 <211> 1659

<212> DNA

<213> Homo sapiens

<400> 140

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305/346

ctgctgttct tctgggtaac caagaggaag ttggaggtgc cgacgggacc tgaagtgcag 120
accctaagc cttcggacgc tgactgggac gacctgtggg accagtttga tgagcggcgg 180
tatctgaatg ccaaaaagtg gcgcgttggg gacgaccctc ataagctgta tgctttcaac 240
cagcgggaga gtgagcggat ctccagcaat cgggccatcc cggacactcg ccatctgaga 300
5 tgcacactgc tgggtgtattg cacggacctt ccacccacta gcatcatcat caccttccac 360
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catctgatcc gggaaatcat attagtggat gacttcagca atgaccctga tgactgtaaa 480
cagctcatca agttgcccaa ggtgaaatgc ttgcgcaata atgaacggca aggtctggtc 540
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acgagggttg tgtccctgt gatcgatc attaacctgg acaccttcac ctacatcgag 720
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accttggtcc ctggcgcccc agtgggttct gtcctttgca agaattgaga tgaccgacag 1500
25 caatggacca aaactgttc ccacatcgag cacatagcat cccacctctg cctcgataca 1560

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gatatgttcg gtgatggcac cgagaacggc aaggaaatcg tcgtcaaccc atgtgagtcc 1620

tcactcatga gccagcactg ggacatgggtg agctcttga 1659

<210> 141

5 <211> 1961

<212> DNA

<213> Homo sapiens

<220>

10 <221> CDS

<222> (185)..(1372)

<400> 141

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ctgtctggct gtacctcaa gcctggccaa accctgtggt tgaaggagat gccctgactc 180

tgcg atg tca ggg atg gaa gaa tac acc act gtc tca ggt gaa gtt cta 229

Met Ser Gly Met Glu Glu Tyr Thr Thr Val Ser Gly Glu Val Leu

1 5 10 15

20 cag aga tgg aaa att cct tca ttt aag gaa aac cag act ctg tcc atg 277

Gln Arg Trp Lys Ile Pro Ser Phe Lys Glu Asn Gln Thr Leu Ser Met

20 25 30

gga gca gca aca gtg cag agc cgt ggc cag tac agc tgc tct ggg cag 325

Gly Ala Ala Thr Val Gln Ser Arg Gly Gln Tyr Ser Cys Ser Gly Gln

25 35 40 45

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gtg atg tat att cca cag aca ttc aca caa act tca gag act gcc atg 373
 Val Met Tyr Ile Pro Gln Thr Phe Thr Gln Thr Ser Glu Thr Ala Met
 50 55 60
 gtt caa gtc caa gag ctg ttt cca cct cct gtg ctg agt gcc atc ccc 421
 5 Val Gln Val Gln Glu Leu Phe Pro Pro Pro Val Leu Ser Ala Ile Pro
 65 70 75
 tct cct gag ccc cga gag ggt agc ctg gtg acc ctg aga tgt cag aca 469
 Ser Pro Glu Pro Arg Glu Gly Ser Leu Val Thr Leu Arg Cys Gln Thr
 80 85 90 95
 10 aag ctg cac ccc ctg agg tca gcc ttg agg ctc ctt ttc tcc ttc cac 517
 Lys Leu His Pro Leu Arg Ser Ala Leu Arg Leu Leu Phe Ser Phe His
 100 105 110
 aag gac ggc cac acc ttg cag gac agg ggc cct cac cca gaa ctc tgc 565
 Lys Asp Gly His Thr Leu Gln Asp Arg Gly Pro His Pro Glu Leu Cys
 15 115 120 125
 atc ccg gga gcc aag gag gga gac tct ggg ctt tac tgg tgt gag gtg 613
 Ile Pro Gly Ala Lys Glu Gly Asp Ser Gly Leu Tyr Trp Cys Glu Val
 130 135 140
 gcc cct gag ggt ggc cag gtc cag aag cag agc ccc cag ctg gag gtc 661
 20 Ala Pro Glu Gly Gly Gln Val Gln Lys Gln Ser Pro Gln Leu Glu Val
 145 150 155
 aga gtg cag gct cct gta tcc cgt cct gtg ctc act ctg cac cac ggg 709
 Arg Val Gln Ala Pro Val Ser Arg Pro Val Leu Thr Leu His His Gly
 160 165 170 175
 25 cct gct gac cct gct gtg ggg gac atg gtg cag ctc ctc tgt gag gca 757

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Pro Ala Asp Pro Ala Val Gly Asp Met Val Gln Leu Leu Cys Glu Ala
 180 185 190
 cag agg ggc tcc cct ccg atc ctg tat tcc ttc tac ctt gat gag aag 805
 Gln Arg Gly Ser Pro Pro Ile Leu Tyr Ser Phe Tyr Leu Asp Glu Lys
 5 195 200 205
 att gtg ggg aac cac tca gct ccc tgt ggt gga acc acc tcc ctc ctc 853
 Ile Val Gly Asn His Ser Ala Pro Cys Gly Gly Thr Thr Ser Leu Leu
 210 215 220
 ttc cca gtg aag tca gaa cag gat gct ggg aac tac tcc tgc gag gct 901
 10 Phe Pro Val Lys Ser Glu Gln Asp Ala Gly Asn Tyr Ser Cys Glu Ala
 225 230 235
 gag aac agt gtc tcc aga gag agg agt gag ccc aag aag ctg tct ctg 949
 Glu Asn Ser Val Ser Arg Glu Arg Ser Glu Pro Lys Lys Leu Ser Leu
 240 245 250 255
 15 aag ggt tct caa gtc ttg ttc act ccc gcc agc aac tgg ctg gtt cct 997
 Lys Gly Ser Gln Val Leu Phe Thr Pro Ala Ser Asn Trp Leu Val Pro
 260 265 270
 tgg ctt cct gcg agc ctg ctt ggc ctg atg gtt att gct gct gca ctt 1045
 Trp Leu Pro Ala Ser Leu Leu Gly Leu Met Val Ile Ala Ala Ala Leu
 20 275 280 285
 ctg gtt tat gtg aga tcc tgg aga aaa gct ggg ccc ctt cca tcc cag 1093
 Leu Val Tyr Val Arg Ser Trp Arg Lys Ala Gly Pro Leu Pro Ser Gln
 290 295 300
 ata cca ccc aca gct cca ggt gga gag cag tgc cca cta tat gcc aac 1141
 25 Ile Pro Pro Thr Ala Pro Gly Gly Glu Gln Cys Pro Leu Tyr Ala Asn

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	305	310	315	
	gtg cat cac cag aaa ggg aaa gat gaa ggt gtt gtc tac tct gtg gtg	1189		
	Val His His Gln Lys Gly Lys Asp Glu Gly Val Val Tyr Ser Val Val			
	320	325	330	335
5	cat aga acc tca aag agg agt gaa gcc agg tct gct gag ttc acc gtg	1237		
	His Arg Thr Ser Lys Arg Ser Glu Ala Arg Ser Ala Glu Phe Thr Val			
	340	345	350	
	ggg aga aag gac agt tct atc atc tgt gcg gag gtg aga tgc ctg cag	1285		
	Gly Arg Lys Asp Ser Ser Ile Ile Cys Ala Glu Val Arg Cys Leu Gln			
10	355	360	365	
	ccc agt gag gtt tca tcc acg gag gtg aat atg aga agc agg act ctc	1333		
	Pro Ser Glu Val Ser Ser Thr Glu Val Asn Met Arg Ser Arg Thr Leu			
	370	375	380	
	caa gaa ccc ctt agc gac tgt gag gag gtt ctc tgc tag tgatggtgtt	1382		
15	Gln Glu Pro Leu Ser Asp Cys Glu Glu Val Leu Cys			
	385	390	395	
	ctcctatcaa cacacgcca ccccgagtct ccagtgctcc tcaggaagac agtgggggtcc	1442		
	tcaactcttt ctgtgggtcc ttcagttccc aagcccagca tcacagagcc ccctgagccc	1502		
	ttgtcctggt caggagcacc tgaaccctgg gttcttttct tagcagaaga ccaaccaatg	1562		
20	gaatgggaag ggagatgctc ccaccaacac acacacttag gttcaatcag tgacactgga	1622		
	cacataagcc acagatgtct tctttccata caagcatgtt agttcgcccc aatatacata	1682		
	tatatatgaa atagtcatgt gccgcataac aacatttcag tcagtgatag actgcataca	1742		
	caacagtgggt ccataagac tgtaatggag tttaaaaatt cctactgcct agtgatatca	1802		
	tagttgcctt aacatcataa cacaacacat ttctcacgcg tttgtggtga tgctggtaca	1862		
25	aacaagctac agcgccgcta gtcatacata aatatagcac atacaattat gtacagtaca	1922		

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ctatacttga taatgataat aaacaactat gttactggt

1961

<210> 142

<211> 2194

5 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

10 <222> (58)..(1710)

<400> 142

aatcggttcc aaacagcagt taggtcagca gtccgctcag ccgaggcagc tctgttc 57

atg gcg ttc tcg aag ctc ttg gag caa gcc gga ggc gtg ggc ctc ttc 105

15 Met Ala Phe Ser Lys Leu Leu Glu Gln Ala Gly Gly Val Gly Leu Phe

1 5 10 15

cag acc ctg cag gtg ctc acc ttc atc ctc ccc tgc ctc atg ata cct 153

Gln Thr Leu Gln Val Leu Thr Phe Ile Leu Pro Cys Leu Met Ile Pro

20 25 30

20 tcc cag atg ctc ctg gag aac ttc tca gcc gcc atc cca ggc cac cga 201

Ser Gln Met Leu Leu Glu Asn Phe Ser Ala Ala Ile Pro Gly His Arg

35 40 45

tgc tgg aca cac atg ctg gac aat ggc tct gcg gtt tcc aca aac atg 249

Cys Trp Thr His Met Leu Asp Asn Gly Ser Ala Val Ser Thr Asn Met

25 50 55 60

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acc ccc aag gcc ctt ctg acc atc tcc atc ccg cca ggc ccc aac cag 297
 Thr Pro Lys Ala Leu Leu Thr Ile Ser Ile Pro Pro Gly Pro Asn Gln
 65 70 75 80
 ggg ccc cac cag tgc cgc cgc ttc cgc cag cca cag tgg cag ctc ttg 345
 5 Gly Pro His Gln Cys Arg Arg Phe Arg Gln Pro Gln Trp Gln Leu Leu
 85 90 95
 gac ccc aat gcc acg gcc acc agc tgg agc gaa gct gac acg gag ccg 393
 Asp Pro Asn Ala Thr Ala Thr Ser Trp Ser Glu Ala Asp Thr Glu Pro
 100 105 110
 10 tgt gtg gac ggc tgg gtc tat gac cgc agc gtc ttc acc tcc acc atc 441
 Cys Val Asp Gly Trp Val Tyr Asp Arg Ser Val Phe Thr Ser Thr Ile
 115 120 125
 gtg gcc aag tgg gac ctg gtg tgc agc tcc cag ggc ttg aag ccc cta 489
 Val Ala Lys Trp Asp Leu Val Cys Ser Ser Gln Gly Leu Lys Pro Leu
 15 130 135 140
 agc cag tcc atc ttc atg tcc ggg atc ctg gtg ggc tcc ttt atc tgg 537
 Ser Gln Ser Ile Phe Met Ser Gly Ile Leu Val Gly Ser Phe Ile Trp
 145 150 155 160
 ggc ctc ctc tcc tac cgg ttt ggg agg aag ccg atg ctg agc tgg tgc 585
 20 Gly Leu Leu Ser Tyr Arg Phe Gly Arg Lys Pro Met Leu Ser Trp Cys
 165 170 175
 tgc ctg cag ttg gcc gtg gcg ggc acc agc acc atc ttc gcc cca aca 633
 Cys Leu Gln Leu Ala Val Ala Gly Thr Ser Thr Ile Phe Ala Pro Thr
 180 185 190
 25 ttc gtc atc tac tgc ggc ctg cgg ttc gtg gcc gct ttt ggg atg gcc 681

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Phe Val Ile Tyr Cys Gly Leu Arg Phe Val Ala Ala Phe Gly Met Ala
 195 200 205
 ggc atc ttt ctg agt tca ctg aca ctg atg gtg gag tgg acc acg acc 729
 Gly Ile Phe Leu Ser Ser Leu Thr Leu Met Val Glu Trp Thr Thr Thr
 5 210 215 220
 agc agg agg gcg gtc acc atg acg gtg gtg gga tgt gcc ttc agc gca 777
 Ser Arg Arg Ala Val Thr Met Thr Val Val Gly Cys Ala Phe Ser Ala
 225 230 235 240
 ggc cag gcg gcg ctg ggc ggc ctg gcc ttt gcc ctg cgg gac tgg agg 825
 10 Gly Gln Ala Ala Leu Gly Gly Leu Ala Phe Ala Leu Arg Asp Trp Arg
 245 250 255
 act ctc cag ctg gca gca tca gtg ccc ttc ttt gcc atc tcc ctg ata 873
 Thr Leu Gln Leu Ala Ala Ser Val Pro Phe Phe Ala Ile Ser Leu Ile
 260 265 270
 15 tcc tgg tgg ctg cca gaa tcc gcc cgg tgg ctg att att aag ggc aaa 921
 Ser Trp Trp Leu Pro Glu Ser Ala Arg Trp Leu Ile Ile Lys Gly Lys
 275 280 285
 cca gac caa gca ctt cag gag ctc aga aag gtg gcc agg ata aat ggc 969
 Pro Asp Gln Ala Leu Gln Glu Leu Arg Lys Val Ala Arg Ile Asn Gly
 20 290 295 300
 cac aag gag gcc aag aac ctg acc ata gag gtg ctg atg tcc agc gtg 1017
 His Lys Glu Ala Lys Asn Leu Thr Ile Glu Val Leu Met Ser Ser Val
 305 310 315 320
 aag gag gag gtg gcc tct gca aag gag ccg cgg tcg gtg ctg gac ctg 1065
 25 Lys Glu Glu Val Ala Ser Ala Lys Glu Pro Arg Ser Val Leu Asp Leu

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	325	330	335	
	ttc tgc gtg ccc gtg ctc cgc tgg agg agc tgc gcc atg ctg gtg gtg	1113		
	Phe Cys Val Pro Val Leu Arg Trp Arg Ser Cys Ala Met Leu Val Val			
	340	345	350	
5	aat ttc tct cta ttg atc tcc tac tat ggg ctg gtc ttc gac ctg cag	1161		
	Asn Phe Ser Leu Leu Ile Ser Tyr Tyr Gly Leu Val Phe Asp Leu Gln			
	355	360	365	
	agc ctg ggc cgt gac atc ttc ctc ctc cag gcc ctc ttc ggg gcc gtg	1209		
	Ser Leu Gly Arg Asp Ile Phe Leu Leu Gln Ala Leu Phe Gly Ala Val			
10	370	375	380	
	gac ttc ctg ggc cgg gcc acc act gcc ctc ttg ctc agt ttc ctt ggc	1257		
	Asp Phe Leu Gly Arg Ala Thr Thr Ala Leu Leu Leu Ser Phe Leu Gly			
	385	390	395	400
	cgc cgc acc atc cag gcg ggt tcc cag gcc atg gcc ggc ctc gcc att	1305		
15	Arg Arg Thr Ile Gln Ala Gly Ser Gln Ala Met Ala Gly Leu Ala Ile			
	405	410	415	
	cta gcc aac atg ctg gtg ccg caa gat ttg cag acc ctg cgt gtg gtc	1353		
	Leu Ala Asn Met Leu Val Pro Gln Asp Leu Gln Thr Leu Arg Val Val			
	420	425	430	
20	ttt gct gtg ctg gga aag gga tgt ttt ggg ata agc cta acc tgc ctc	1401		
	Phe Ala Val Leu Gly Lys Gly Cys Phe Gly Ile Ser Leu Thr Cys Leu			
	435	440	445	
	acc atc tac aag gct gaa ctc ttt cca acg cca gtg cgg atg aca gca	1449		
	Thr Ile Tyr Lys Ala Glu Leu Phe Pro Thr Pro Val Arg Met Thr Ala			
25	450	455	460	

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gat ggc att ctg cat aca gtg ggc cgg ctg ggg gct atg atg ggt ccc 1497
 Asp Gly Ile Leu His Thr Val Gly Arg Leu Gly Ala Met Met Gly Pro
 465 470 475 480
 ctg atc ctg atg agc cgc caa gcc ctg ccc ctg ctg cct cct ctc ctc 1545
 5 Leu Ile Leu Met Ser Arg Gln Ala Leu Pro Leu Leu Pro Pro Leu Leu
 485 490 495
 tat ggc gtt atc tcc att gct tcc agc ctg gtt gtg ctg ttc ttc ctc 1593
 Tyr Gly Val Ile Ser Ile Ala Ser Ser Leu Val Val Leu Phe Phe Leu
 500 505 510
 10 ccg gag acc cag gga ctt ccg ctc cct gac act atc cag gac ctg gag 1641
 Pro Glu Thr Gln Gly Leu Pro Leu Pro Asp Thr Ile Gln Asp Leu Glu
 515 520 525
 agc cag aaa tca aca gca gcc cag ggc aac cgg caa gag gcc gtc act 1689
 Ser Gln Lys Ser Thr Ala Ala Gln Gly Asn Arg Gln Glu Ala Val Thr
 15 530 535 540
 gtg gaa agt acc tcg ctc tag aaattgtgcc tgcattggagc ccctttagtc 1740
 Val Glu Ser Thr Ser Leu
 545 550
 aaagactcct ggaaaggagt tgcctcttct ccaatcagag cgtggaggcg agttgggcga 1800
 20 cttcaagggc ctggcatggc agaggccagg cagccgtggc cgagtggaca gcgtggccgt 1860
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 gacgggttccc ctccctttcc ctgccaggct catgtcttta caccttcaact cagccacgcc 2040
 aaccagagac tgggttccaa tctcacccca ccacatacag agccctcatc tgtgaaatga 2100
 25 gaatgatcac gtgaccacc cccaggggca ggtatcaggg tgaactgac ttagcaccgg 2160

315/346

ccaaataaat ggaacctgct gagagagctg ccag

2194

<210> 143

<211> 2753

5 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

10 <222> (109)..(765)

<400> 143

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ggcttgtctg ttccctcctg agcctgagcc ccttaccttc ctgacccc atg aag cac 117

15

Met Lys His

1

aca ctg gct ctg ctg gct ccc ctg ctg ggc ctg ggc ctg ggg ctg gcc 165

Thr Leu Ala Leu Leu Ala Pro Leu Leu Gly Leu Gly Leu Gly Leu Ala

5

10

15

20 ctg agt cag ctg gct gca ggg gcc aca gac tgc aag ttc ctt ggc ccg 213

Leu Ser Gln Leu Ala Ala Gly Ala Thr Asp Cys Lys Phe Leu Gly Pro

20

25

30

35

gca gag cac ctg aca ttc acc cca gca gcc agg gcc cgg tgg ctg gcc 261

Ala Glu His Leu Thr Phe Thr Pro Ala Ala Arg Ala Arg Trp Leu Ala

25

40

45

50

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	cct cga gtt cgt gcg cca gga ctc ctg gac tcc ctc tat ggc acc gtg	309
	Pro Arg Val Arg Ala Pro Gly Leu Leu Asp Ser Leu Tyr Gly Thr Val	
	55 60 65	
	cgc cgc ttc ctc tcg gtg gtg cag ctc aat cct ttc cct tca gag ttg	357
5	Arg Arg Phe Leu Ser Val Val Gln Leu Asn Pro Phe Pro Ser Glu Leu	
	70 75 80	
	gta aag gcc cta ctg aat gag ctg gcc tcc gtg aag gtg aat gag gtg	405
	Val Lys Ala Leu Leu Asn Glu Leu Ala Ser Val Lys Val Asn Glu Val	
	85 90 95	
10	gtg cgg tac gag gcg ggc tac gtg gta tgc gct gtg atc gcg ggc ctc	453
	Val Arg Tyr Glu Ala Gly Tyr Val Val Cys Ala Val Ile Ala Gly Leu	
	100 105 110 115	
	tac ctg ctg ctg gtg ccc act gcc ggg ctt tgc ttc tgc tgc tgc cgc	501
	Tyr Leu Leu Leu Val Pro Thr Ala Gly Leu Cys Phe Cys Cys Cys Arg	
15	120 125 130	
	tgc cac cgg cgc tgc ggg gga cga gtg aag aca gag cac aag gcg ctg	549
	Cys His Arg Arg Cys Gly Gly Arg Val Lys Thr Glu His Lys Ala Leu	
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	gcc tgt gag cgc gcg gcc ctc atg gtc ttc ctg ctg ctg acc acc ctc	597
20	Ala Cys Glu Arg Ala Ala Leu Met Val Phe Leu Leu Leu Thr Thr Leu	
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	ttg ctg ctg att ggt gtg gtc tgt gcc ttt gtc acc aac cag cgc acg	645
	Leu Leu Leu Ile Gly Val Val Cys Ala Phe Val Thr Asn Gln Arg Thr	
	165 170 175	
25	cat gaa cag atg ggc ccc agc atc gag gcc atg cct gag acc ctg ctc	693

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His Glu Gln Met Gly Pro Ser Ile Glu Ala Met Pro Glu Thr Leu Leu
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 agc ctc tgg ggc ctg gtc tct gat gtc ccc caa gtg agc act gtt acc 741
 Ser Leu Trp Gly Leu Val Ser Asp Val Pro Gln Val Ser Thr Val Thr
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 cct cac cct cat gtg ccc ctg tga gactgggcc cgggcaggac agagccgagt 795
 Pro His Pro His Val Pro Leu
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 gggccctcga tggcccataa ccagcgcatac tgaaagccgc ctctctctccc gcccttgcct 855
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25 <222> (42) .. (1832)

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Met Ala Ala Asn Ser

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1

5

acc agc gac ctc cac act ccc ggg acg cag ctg agc gtg gct gac atc 104

Thr Ser Asp Leu His Thr Pro Gly Thr Gln Leu Ser Val Ala Asp Ile

10

15

20

atc gtc atc act gtg tat ttt gct ctg aat gtg gcc gtg ggc ata tgg 152

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Ile Val Ile Thr Val Tyr Phe Ala Leu Asn Val Ala Val Gly Ile Trp

25

30

35

tcc tct tgt cgg gcc agt agg aac acg gtg aat ggc tac ttc ctg gca 200

Ser Ser Cys Arg Ala Ser Arg Asn Thr Val Asn Gly Tyr Phe Leu Ala

40

45

50

15

ggc cgg gac atg acg tgg tgg ccg att gga gcc tcc ctc ttc gcc agc 248

Gly Arg Asp Met Thr Trp Trp Pro Ile Gly Ala Ser Leu Phe Ala Ser

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60

65

agc gag ggc tct ggc ctc ttc att gga ctg gcg ggc tca ggc gcg gca 296

Ser Glu Gly Ser Gly Leu Phe Ile Gly Leu Ala Gly Ser Gly Ala Ala

20

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80

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Gly Gly Leu Ala Val Ala Gly Phe Glu Trp Asn Ala Thr Tyr Val Leu

90

95

100

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25

Leu Ala Leu Ala Trp Val Phe Val Pro Ile Tyr Ile Ser Ser Glu Ile

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	105	110	115	
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	Val Thr Leu Pro Glu Tyr Ile Gln Lys Arg Tyr Gly Gly Gln Arg Ile			
	120	125	130	
5	cgc atg tac ctg tct gtc ctg tcc ctg cta ctg tct gtc ttc acc aag	488		
	Arg Met Tyr Leu Ser Val Leu Ser Leu Leu Leu Ser Val Phe Thr Lys			
	135	140	145	
	ata tcg ctg gac ctg tac gcg ggg gct ctg ttt gtg cac atc tgc ctg	536		
	Ile Ser Leu Asp Leu Tyr Ala Gly Ala Leu Phe Val His Ile Cys Leu			
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	ggc tgg aac ttc tac ctc tcc acc atc ctc acg ctc ggc atc aca gcc	584		
	Gly Trp Asn Phe Tyr Leu Ser Thr Ile Leu Thr Leu Gly Ile Thr Ala			
	170	175	180	
	ctg tac acc atc gca ggg ggc ctg gct gct gta atc tac acg gac gcc	632		
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	185	190	195	
	ctg cag acg ctc atc atg gtg gtg ggg gct gtc atc ctg aca atc aaa	680		
	Leu Gln Thr Leu Ile Met Val Val Gly Ala Val Ile Leu Thr Ile Lys			
	200	205	210	
20	gct ttt gac cag atc ggt ggt tac ggg cag ctg gag gca gcc tac gcc	728		
	Ala Phe Asp Gln Ile Gly Gly Tyr Gly Gln Leu Glu Ala Ala Tyr Ala			
	215	220	225	
	cag gcc att ccc tcc agg acc att gcc aac acc acc tgc cac ctg cca	776		
	Gln Ala Ile Pro Ser Arg Thr Ile Ala Asn Thr Thr Cys His Leu Pro			
25	230	235	240	245

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	cgt aca gac gcc atg cac atg ttt cga gac ccc cac aca ggg gac ctg	824
	Arg Thr Asp Ala Met His Met Phe Arg Asp Pro His Thr Gly Asp Leu	
	250 255 260	
	ccg tgg acc ggg atg acc ttt ggc ctg acc atc atg gcc acc tgg tac	872
5	Pro Trp Thr Gly Met Thr Phe Gly Leu Thr Ile Met Ala Thr Trp Tyr	
	265 270 275	
	tgg tgc acc gac cag gtc atc gtg cag cga tca ctg tca gcc cgg gac	920
	Trp Cys Thr Asp Gln Val Ile Val Gln Arg Ser Leu Ser Ala Arg Asp	
	280 285 290	
10	ctg aac cat gcc aag gcg ggc tcc atc ctg gcc agc tac ctc aag atg	968
	Leu Asn His Ala Lys Ala Gly Ser Ile Leu Ala Ser Tyr Leu Lys Met	
	295 300 305	
	ctc ccc atg ggc ctg atc ata atg ccg ggc atg atc agc cgc gca ttg	1016
	Leu Pro Met Gly Leu Ile Ile Met Pro Gly Met Ile Ser Arg Ala Leu	
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	ttc cca gat gat gtg ggc tgc gtg gtg ccg tcc gag tgc ctg cgg gcc	1064
	Phe Pro Asp Asp Val Gly Cys Val Val Pro Ser Glu Cys Leu Arg Ala	
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	tgc ggg gcc gag gtc ggc tgc tcc aac atc gcc tac ccc aag ctg gtc	1112
20	Cys Gly Ala Glu Val Gly Cys Ser Asn Ile Ala Tyr Pro Lys Leu Val	
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	atg gaa ctg atg ccc atc ggt ctg cgg ggg ctg atg atc gca gtg atg	1160
	Met Glu Leu Met Pro Ile Gly Leu Arg Gly Leu Met Ile Ala Val Met	
	360 365 370	
25	ctg gcg gcg ctc atg tcg tcg ctg acc tcc atc ttc aac agc agc agc	1208

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Leu Ala Ala Leu Met Ser Ser Leu Thr Ser Ile Phe Asn Ser Ser Ser
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 Thr Leu Phe Thr Met Asp Ile Trp Arg Arg Leu Arg Pro Arg Ser Gly
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 Glu Arg Glu Leu Leu Leu Val Gly Arg Leu Val Ile Val Ala Leu Ile
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 Gln Leu Phe Ile Tyr Met Gln Ser Val Thr Ser Ser Leu Ala Pro Pro
 440 445 450
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 Val Thr Ala Val Phe Val Leu Gly Val Phe Trp Arg Arg Ala Asn Glu
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 Gln Gly Ala Phe Trp Gly Leu Ile Ala Gly Leu Val Val Gly Ala Thr
 20 470 475 480 485
 agg ctg gtc ctg gaa ttc ctg aac cca gcc cca ccg tgc gga gag cca 1544
 Arg Leu Val Leu Glu Phe Leu Asn Pro Ala Pro Pro Cys Gly Glu Pro
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 gac acg cgg cca gcc gtc ctg ggg agc atc cac tac ctg cac ttc gct 1592
 25 Asp Thr Arg Pro Ala Val Leu Gly Ser Ile His Tyr Leu His Phe Ala

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	505	510	515	
	gtc gcc ctc ttt gca ctc agt ggt gct gtt gtg gtg gct gga agc ctg	1640		
	Val Ala Leu Phe Ala Leu Ser Gly Ala Val Val Val Ala Gly Ser Leu			
	520	525	530	
5	ctg acc cca ccc cca cag agt gtc cag att gag aac ctt acc tgg tgg	1688		
	Leu Thr Pro Pro Pro Gln Ser Val Gln Ile Glu Asn Leu Thr Trp Trp			
	535	540	545	
	acc ctg gct cag gat gtg ccc ttg gga act aaa gca ggt gat ggc caa	1736		
	Thr Leu Ala Gln Asp Val Pro Leu Gly Thr Lys Ala Gly Asp Gly Gln			
10	550	555	560	565
	aca ccc cag aaa cac gcc ttc tgg gcc cgt gtc tgt ggc ttc aat gcc	1784		
	Thr Pro Gln Lys His Ala Phe Trp Ala Arg Val Cys Gly Phe Asn Ala			
	570	575	580	
	atc ctc ctc atg tgt gtc aac ata ttc ttt tat gcc tac ttc gcc tga	1832		
15	Ile Leu Leu Met Cys Val Asn Ile Phe Phe Tyr Ala Tyr Phe Ala			
	585	590	595	
	cactgccatc ctggacagaa aggcaggagc tctgagtcct caggtccacc catttcctc	1892		
	atggggatcc cgaagcccca agaggggcag attcccctca cagctgcaca gcagctcggg	1952		
	gccaagaac tggccaagcc agcaaagcgg gagccctgaa aaattagggg ggaaatggga	2012		
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324/346

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<220>

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                                     1           5
ctg ggg cta ctg ctg ttg ctg ccg ctg gct ggc cac ttg gct ctg ggt 162
Leu Gly Leu Leu Leu Leu Pro Leu Ala Gly His Leu Ala Leu Gly
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15 gcc cag cag ggt cgt ggg cgc cgg gag cta gca ccg ggt ctg cac ctg 210
Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala Pro Gly Leu His Leu
                                     25           30           35
cgg ggc atc cgg gac gcg gga ggc cgg tac tgc cag gag cag gac ctg 258
Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys Gln Glu Gln Asp Leu
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tgc tgc cgc ggc cgt gcc gac gac tgt gcc ctg ccc tac ctg ggc gcc 306
Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu Pro Tyr Leu Gly Ala
           55           60           65
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25 Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr Val Ser Asp Cys Cys

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	90	95	100		
5	atc caa gga tgt atg cat gga ggt cgt atc tat cca gtc ttg gga acg	450			
	Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr Pro Val Leu Gly Thr				
	105	110	115		
	tac tgg gac aac tgt aac cgt tgc acc tgc cag gag aac agg cag tgg	498			
	Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln Glu Asn Arg Gln Trp				
10	120	125	130		
	cag tgt gac caa gaa cca tgc ctg gtg gat cca gac atg atc aaa gcc	546			
	Gln Cys Asp Gln Glu Pro Cys Leu Val Asp Pro Asp Met Ile Lys Ala				
	135	140	145		
	atc aac cag ggc aac tat ggc tgg cag gct ggg aac cac agc gcc ttc	594			
15	Ile Asn Gln Gly Asn Tyr Gly Trp Gln Ala Gly Asn His Ser Ala Phe				
	150	155	160	165	
	tgg ggc atg acc ctg gat gag ggc att cgc tac cgc ctg ggc acc atc	642			
	Trp Gly Met Thr Leu Asp Glu Gly Ile Arg Tyr Arg Leu Gly Thr Ile				
	170	175	180		
20	cgc cca tct tcc tcg gtc atg aac atg cat gaa att tat aca gtg ctg	690			
	Arg Pro Ser Ser Ser Val Met Asn Met His Glu Ile Tyr Thr Val Leu				
	185	190	195		
	aac cca ggg gag gtg ctt ccc aca gcc ttc gag gcc tct gag aag tgg	738			
	Asn Pro Gly Glu Val Leu Pro Thr Ala Phe Glu Ala Ser Glu Lys Trp				
25	200	205	210		

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 tgg gcc ttc tcc aca gca gct gtg gca tcc gat cgt gtc tca atc cat 834
 5 Trp Ala Phe Ser Thr Ala Ala Val Ala Ser Asp Arg Val Ser Ile His
 230 235 240 245
 tct ctg gga cac atg acg cct gtc ctg tcg ccc cag aac ctg ctg tct 882
 Ser Leu Gly His Met Thr Pro Val Leu Ser Pro Gln Asn Leu Leu Ser
 250 255 260
 10 tgt gac acc cac cag cag cag ggc tgc cgc ggt ggg cgt ctc gat ggt 930
 Cys Asp Thr His Gln Gln Gln Gly Cys Arg Gly Gly Arg Leu Asp Gly
 265 270 275
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 25 cct gtc tac cgc ctc ggc tcc aac gac aag gag atc atg aag gag ctg 1170

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Pro Val Tyr Arg Leu Gly Ser Asn Asp Lys Glu Ile Met Lys Glu Leu
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gcccgtcct gtccccgaca tcacgtgtat tccgcacgtc ccctccgcgc tgtgtgtcta 180
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 Met Ala Gly Ser Asp Thr Ala Pro Phe Leu Ser Gln Ala
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 30 35 40 45
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 Gly Leu Gln Arg Ile Thr Gly Leu Ser Pro Gly Arg Ser Ala Leu Ile
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 gac agt agc tct ggg ctc atc cag acc gtg ttc atc tcc agt tac atg 697
 Asp Ser Ser Ser Gly Leu Ile Gln Thr Val Phe Ile Ser Ser Tyr Met
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 gtg ttg gca cct gtg ttt ggc tac ctg ggt gac agg tac aat cgg aag 745
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130	135	140		
5 tca tcc ttc atc ccc gga gag cat ttc tgg ctg ctc ctc ctg acc cgg	841			
Ser Ser Phe Ile Pro Gly Glu His Phe Trp Leu Leu Leu Leu Thr Arg				
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10 160	165	170		
ctc att gcc gac ctc ttt gtg gcc gac cag cgg agc cgg atg ctc agc	937			
Leu Ile Ala Asp Leu Phe Val Ala Asp Gln Arg Ser Arg Met Leu Ser				
175	180	185		
atc ttc tac ttt gcc att ccg gtg ggc agt ggt ctg ggc tac att gca	985			
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Val Arg Glu Pro Pro Arg Gly Ala Val Glu Arg His Ser Asp Leu Pro				
25 240	245	250		

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ccc ctg aac ccc acc tcg tgg tgg gca gat ctg agg gct ctg gca aga 1177
 Pro Leu Asn Pro Thr Ser Trp Trp Ala Asp Leu Arg Ala Leu Ala Arg
 255 260 265
 aat ctc atc ttt gga ctc atc acc tgc ctg acc gga gtc ctg ggt gtg 1225
 5 Asn Leu Ile Phe Gly Leu Ile Thr Cys Leu Thr Gly Val Leu Gly Val
 270 275 280 285
 ggc ctg ggt gtg gag atc agc cgc cgg ctc cgc cac tcc aac ccc cgg 1273
 Gly Leu Gly Val Glu Ile Ser Arg Arg Leu Arg His Ser Asn Pro Arg
 290 295 300
 10 gct gat ccc ctg gtc tgt gcc act ggc ctc ctg ggc tct gca ccc ttc 1321
 Ala Asp Pro Leu Val Cys Ala Thr Gly Leu Leu Gly Ser Ala Pro Phe
 305 310 315
 ctc ttc ctg tcc ctt gcc tgc gcc cgt ggt agc atc gtg gcc act tat 1369
 Leu Phe Leu Ser Leu Ala Cys Ala Arg Gly Ser Ile Val Ala Thr Tyr
 15 320 325 330
 att ttc atc ttc att gga gag acc ctc ctg tcc atg aac tgg gcc atc 1417
 Ile Phe Ile Phe Ile Gly Glu Thr Leu Leu Ser Met Asn Trp Ala Ile
 335 340 345
 gtg gcc gac att ctg ctg tac gtg gtg atc cct acc cga cgc tcc acc 1465
 20 Val Ala Asp Ile Leu Leu Tyr Val Val Ile Pro Thr Arg Arg Ser Thr
 350 355 360 365
 gcc gag gcc ttc cag atc gtg ctg tcc cac ctg ctg ggt gat gct ggg 1513
 Ala Glu Ala Phe Gln Ile Val Leu Ser His Leu Leu Gly Asp Ala Gly
 370 375 380
 25 agc ccc tac ctc att ggc ctg atc tct gac cgc ctg cgc cgg aac tgg 1561

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Ser Pro Tyr Leu Ile Gly Leu Ile Ser Asp Arg Leu Arg Arg Asn Trp
 385 390 395
 ccc ccc tcc ttc ttg tcc gag ttc cgg gct ctg cag ttc tcg ctc atg 1609
 Pro Pro Ser Phe Leu Ser Glu Phe Arg Ala Leu Gln Phe Ser Leu Met
 5 400 405 410
 ctc tgc gcg ttt gtt ggg gca ctg ggc ggc gca gcc ttc ctg ggc acc 1657
 Leu Cys Ala Phe Val Gly Ala Leu Gly Gly Ala Ala Phe Leu Gly Thr
 415 420 425
 gcc atc ttc att gag gcc gac cgc cgg cgg gca cag ctg cac gtg cag 1705
 10 Ala Ile Phe Ile Glu Ala Asp Arg Arg Arg Ala Gln Leu His Val Gln
 430 435 440 445
 ggc ctg ctg cac gaa gca ggg tcc aca gac gac cgg att gtg gtg ccc 1753
 Gly Leu Leu His Glu Ala Gly Ser Thr Asp Asp Arg Ile Val Val Pro
 450 455 460
 15 cag cgg ggc cgc tcc acc cgc gtg ccc gtg gcc agt gtg ctc atc tga 1801
 Gln Arg Gly Arg Ser Thr Arg Val Pro Val Ala Ser Val Leu Ile
 465 470 475
 gaggtctccg ctcacctacc tgcacatctg ccacagctgg ccctgggccc accccacgaa 1861
 gggcctgggc ctaaccctt ggctggccc agcttccaga gggaccctgg gccgtgtgcc 1921
 20 agctcccaga cactacatgg gtagctcagg ggaggagggtg ggggtccagg agggggatcc 1981
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 25 <211> 2176

333/346

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<213> Homo sapiens

<220>

5 <221> CDS

<222> (263)..(1612)

<400> 147

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caggcgccgg caggcgcca agcgccggg tgccgcagcc caggccggg tcgcgcctct 180
ttgtttccac gggtagcggc gcagtcccgg gcccggggcg gaagtgcagc gcgctcggcg 240
cgggggccgc ggcgccgcca cc atg agc gac atc cgc cac tcg ctg ctg cgc 292
Met Ser Asp Ile Arg His Ser Leu Leu Arg
15 1 5 10
cgc gat gcg ctg agc gcc gcc aag gag gtg ttg tac cac ctg gac atc 340
Arg Asp Ala Leu Ser Ala Ala Lys Glu Val Leu Tyr His Leu Asp Ile
15 20 25
tac ttc agc agc cag ctg cag agc gcg ccg ctg ccc atc gtg gac aag 388
20 Tyr Phe Ser Ser Gln Leu Gln Ser Ala Pro Leu Pro Ile Val Asp Lys
30 35 40
ggc ccc gtg gag ctg ctg gag gag ttc gtg ttc cag gtg ccc aag gag 436
Gly Pro Val Glu Leu Leu Glu Glu Phe Val Phe Gln Val Pro Lys Glu
45 50 55
25 cgc agc gcg cag ccc aag aga ctg aat tcc ctt cag gag ctt caa ctt 484

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Arg Ser Ala Gln Pro Lys Arg Leu Asn Ser Leu Gln Glu Leu Gln Leu
 60 65 70
 ctt gaa atc atg tgc aat tat ttc cag gag caa acc aag gac tct gtt 532
 Leu Glu Ile Met Cys Asn Tyr Phe Gln Glu Gln Thr Lys Asp Ser Val
 5 75 80 85 90
 cgg cag att att ttt tca tcc ctt ttc agc cct caa ggg aac aaa gcc 580
 Arg Gln Ile Ile Phe Ser Ser Leu Phe Ser Pro Gln Gly Asn Lys Ala
 95 100 105
 gat gac agc cgg atg agc ttg ttg gga aaa ctg gtc tcc atg gcg gtg 628
 10 Asp Asp Ser Arg Met Ser Leu Leu Gly Lys Leu Val Ser Met Ala Val
 110 115 120
 gct gtg tgt cga atc ccg gtg ttg gag tgt gct gcc tcc tgg ctt cag 676
 Ala Val Cys Arg Ile Pro Val Leu Glu Cys Ala Ala Ser Trp Leu Gln
 125 130 135
 15 cgg acg ccc gtg gtt tac tgt gtg agg tta gcc aag gcc ctt gta gat 724
 Arg Thr Pro Val Val Tyr Cys Val Arg Leu Ala Lys Ala Leu Val Asp
 140 145 150
 gac tac tgc tgt ttg gtg ccg gga tcc att cag acg ctg aag cag ata 772
 Asp Tyr Cys Cys Leu Val Pro Gly Ser Ile Gln Thr Leu Lys Gln Ile
 20 155 160 165 170
 ttc agt gcc agc ccg aga ttc tgc tgc cag ttc atc acc tcc gtt acc 820
 Phe Ser Ala Ser Pro Arg Phe Cys Cys Gln Phe Ile Thr Ser Val Thr
 175 180 185
 gcg ctc tat gac ctg tca tca gat gac ctc att cca cct atg gac ttg 868
 25 Ala Leu Tyr Asp Leu Ser Ser Asp Asp Leu Ile Pro Pro Met Asp Leu

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	190	195	200	
	ctt gaa atg att gtc acc tgg att ttt gag gac cca agg ttg att ctc			916
	Leu Glu Met Ile Val Thr Trp Ile Phe Glu Asp Pro Arg Leu Ile Leu			
	205	210	215	
5	atc act ttt tta aat act ccg att gcg gcc aat ctg cca ata gga ttc			964
	Ile Thr Phe Leu Asn Thr Pro Ile Ala Ala Asn Leu Pro Ile Gly Phe			
	220	225	230	
	tta gag ctc acc ccg ctc gtt gga ttg atc cgc tgg tgc gtg aag gca			1012
	Leu Glu Leu Thr Pro Leu Val Gly Leu Ile Arg Trp Cys Val Lys Ala			
10	235	240	245	250
	ccc ctg gct tat aaa agg aaa aag aag ccc ccc tta tcc aat ggc cat			1060
	Pro Leu Ala Tyr Lys Arg Lys Lys Lys Pro Pro Leu Ser Asn Gly His			
	255	260	265	
	gtc agc aac aag gtc aca aag gac ccg ggc gtg ggg atg gac aga gac			1108
15	Val Ser Asn Lys Val Thr Lys Asp Pro Gly Val Gly Met Asp Arg Asp			
	270	275	280	
	tcc cac ctc ttg tac tca aaa ctc cac ctc agc gtc ctg caa gtg ctc			1156
	Ser His Leu Leu Tyr Ser Lys Leu His Leu Ser Val Leu Gln Val Leu			
	285	290	295	
20	atg acg ctg cag ctg cac ctg acc gag aag aat ctg tat ggg cgc ctg			1204
	Met Thr Leu Gln Leu His Leu Thr Glu Lys Asn Leu Tyr Gly Arg Leu			
	300	305	310	
	ggg ctg atc ctc ttc gac cac atg gtc ccg ctg gta gag gag atc aac			1252
	Gly Leu Ile Leu Phe Asp His Met Val Pro Leu Val Glu Glu Ile Asn			
25	315	320	325	330

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agg ttg gcg gat gaa ctg aac ccc ctc aac gcc tcc cag gag att gag 1300
 Arg Leu Ala Asp Glu Leu Asn Pro Leu Asn Ala Ser Gln Glu Ile Glu
 335 340 345
 ctc tcg ctg gac cgg ctg gcg cag gct ctg cag gtg gcc atg gcc tca 1348
 5 Leu Ser Leu Asp Arg Leu Ala Gln Ala Leu Gln Val Ala Met Ala Ser
 350 355 360
 gga gct ctg ctg tgc acg aga gat gac ctg aga acc ttg tgc tcc agg 1396
 Gly Ala Leu Leu Cys Thr Arg Asp Asp Leu Arg Thr Leu Cys Ser Arg
 365 370 375
 10 ctg ccc cat aat aac ctc ctc cag ctg gtg atc tcg ggt ccc gtg cag 1444
 Leu Pro His Asn Asn Leu Leu Gln Leu Val Ile Ser Gly Pro Val Gln
 380 385 390
 cag tcg cct cac gcc gcg ctc ccc ccg ggg ttc tac ccc cac atc cac 1492
 Gln Ser Pro His Ala Ala Leu Pro Pro Gly Phe Tyr Pro His Ile His
 15 395 400 405 410
 acg ccc ccg ctg ggc tac ggg gct gtc ccg gcc cac ccc gcc gcc cac 1540
 Thr Pro Pro Leu Gly Tyr Gly Ala Val Pro Ala His Pro Ala Ala His
 415 420 425
 ccc gcc ctg ccc acg cac ccc ggc cac acc ttc atc tcc ggc gtg acc 1588
 20 Pro Ala Leu Pro Thr His Pro Gly His Thr Phe Ile Ser Gly Val Thr
 430 435 440
 ttt ccc ttc agg ccc atc cgc tag gctggccgt gtgtgccttc tgcgtctctg 1642
 Phe Pro Phe Arg Pro Ile Arg
 445 450
 25 ctggacgaag cctttcgaga tggaaggggt ggccggactc ccagaagaga acctcgggga 1702

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aggggtcggg cagcccctcc ccgccggcag aaccgtcttg gtgtcacgga gtccaggtgc 1762
ttcccacccg gtcgcattct ttgacatgca gattggatgg tggaggggaag agtccagcct 1822
ctgccgagag cctgctgcgt gcatttttaa aagatgccga tcctggggagc ctctgttctc 1882
tgcgcatttc agacacagcc tgtgtggcga ggagtgtgac ggcaggagcc acgggtgcaa 1942
5 gcccgtgtgt ctggcctctt tcctcgtgaa gacgatgtgt ccccgccaga aaaagtgggc 2002
tccttctgca gcccgtgag ctgagcccag gctgcgtagt gaccacaagc ttatgtgcag 2062
cactgctcag ggaggctgtc aggaattccc ctcacctcgg aaaggaactt ctcagtttta 2122
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10 <210> 148
<211> 1363
<212> DNA
<213> Homo sapiens

15 <220>
<221> CDS
<222> (16)..(333)

<400> 148

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Met Arg Arg Ile Ser Leu Thr Ser Ser Pro Val Arg
1 5 10
ctt ctt ttg ttt ctg ctg ttg cta cta ata gcc ttg gag atc atg gtt 99
Leu Leu Leu Phe Leu Leu Leu Leu Leu Ile Ala Leu Glu Ile Met Val
25 15 20 25

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ggt ggt cac tct ctt tgc ttc aac ttc act ata aaa tca ttg tcc aga 147
 Gly Gly His Ser Leu Cys Phe Asn Phe Thr Ile Lys Ser Leu Ser Arg
 30 35 40
 cct gga cag ccc tgg tgt gaa gcg cag gtc ttc ttg aat aaa aat ctt 195
 5 Pro Gly Gln Pro Trp Cys Glu Ala Gln Val Phe Leu Asn Lys Asn Leu
 45 50 55 60
 ttc ctt cag tac aac agt gac aac aac atg gtc aaa cct ctg ggc ctc 243
 Phe Leu Gln Tyr Asn Ser Asp Asn Asn Met Val Lys Pro Leu Gly Leu
 65 70 75
 10 ctg ggg aag aag gta aat gcc acc agc act tgg gga gaa aac cca aac 291
 Leu Gly Lys Lys Val Asn Ala Thr Ser Thr Trp Gly Glu Asn Pro Asn
 80 85 90
 gct ggg aga agt ggg gcg aga cct cag gat gct cct ttg tga 333
 Ala Gly Arg Ser Gly Ala Arg Pro Gln Asp Ala Pro Leu
 15 95 100 105
 catcaaacc cagataaaga ccagtgatcc ttccactctg caagtcgaga tgttttgtca 393
 acgtgaagca gaacggtgca ctggtgcatc ctggcagttc gccaccaatg gagagaaatc 453
 cctcctcttt gacgcaatga acatgacctg gacagtaatt aatcatgaag ccagtaagat 513
 caaggagaca tggaagaaag acagagggct ggaaaagtat ttcaggaagc tctcaaagg 573
 20 agactgcgat cactggctca gggaattctt agggcactgg gaggcaatgc cagaaccgac 633
 aggcagaaga tccacctaga ggtgatacca cggcggcgca gagttgttca cctgtggtcc 693
 togatcgctg acagccttgg ctcccactgc tgtgtgttcc ctgagtcaag tggaggcgga 753
 gcctgcaatg agcggagatc ggcctctgctc attccagtct tggcaacaga gcaagactcc 813
 gtctcaaaaa aaaaaatttt ttttcagtac atatttttta aaagataggg ctgggcacag 873
 25 cagctcacat ctataatccc aacactttgg gaggcctagg caggaggatc acttgagccc 933

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aggaatctga agctgcagtg agcctttgct cgtgagattg tggacctatg atcctaccac 993
 cagcccacct ggttctaaca cccctctctc tatgtgtgag agggagagaa gaaaagtgag 1053
 ggagaaaaga gagataagca aagaacagag aggaaaaatg gaaaataaga ggaaattggg 1113
 ggaattaaac agagggggagg gcatggatcc cggggagtta gaagagtagc agcttgtgga 1173
 5 ttactacgca gtggaggaag aagagttggt ggaaattatt tgagaggtag tataatcatt 1233
 tgtgaggcag ttttctgcat tcaccatttc tcacagacta agttactcat aagcaaactg 1293
 gcaattcaca ttacactgaa attcttcctt aatacatcat ttgcattgga ataaagtacg 1353
 gttttcaaac 1363

10 <210> 149
 <211> 1043
 <212> DNA
 <213> Homo sapiens

15 <220>
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 <222> (227)..(472)

<400> 149
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 gcgcaccaca gatactaaca gtcgtcttca caggcgaccg tagaccacac atactaacag 120
 tcgtcttcac aggcgaccac gcaccacaca cactaacagt cgtcttcaca ggcgaccgcg 180
 caccacacac actaacggac gtgcccgaca tcttcacagg cacagc atg agc cct 235

Met Ser Pro

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gat gtg cgc ttt ctg ctc ctg ctc ctg ctc ctg ccc ctt cgg agg cct 283
 Asp Val Arg Phe Leu Leu Leu Leu Leu Leu Leu Pro Leu Arg Arg Pro
 5 10 15
 gtg cca gtg gca gct ggg ccc gga gac acc agg ccg gca ctg ctc tct 331
 5 Val Pro Val Ala Ala Gly Pro Gly Asp Thr Arg Pro Ala Leu Leu Ser
 20 25 30 35
 ttc gag gca ccc gtg ttt gtg ccg acg ctg act ccc ggt tgt ctg cag 379
 Phe Glu Ala Pro Val Phe Val Pro Thr Leu Thr Pro Gly Cys Leu Gln
 40 45 50
 10 cag cca cgt ggc cga aat gga gcc tct cca cgg ggg ctc ctt ccc cag 427
 Gln Pro Arg Gly Arg Asn Gly Ala Ser Pro Arg Gly Leu Leu Pro Gln
 55 60 65
 ccc ctg gat ggc aca gca gcc tct cct gtc tgt cac cac gtg tga 472
 Pro Leu Asp Gly Thr Ala Ala Ser Pro Val Cys His His Val
 15 70 75 80
 cctgctccct tagtcttcag ccgctcatcc acgtctgcag gggcatctaa ctctgtccca 532
 gggatatcca gaccctggct cagcggccag gctctccatt caggctccat cgtccacctc 592
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 20 gcacctgccc atccggcacc atcctctgat ccagggactg tgagcaacag ggccccgtgg 772
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 gtgctgaact gcccaataaa tccacaagta agagttgcaa gaaggagcca aaaagggctg 892
 agctgaatga ctcatatatg aaataatttg ataattaata taaataggaa atttaaagtc 952
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 25 acctataatt gcaaaataaa agcattgaaa g 1043

341/346

<210> 150

<211> 2435

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5 <213> Homo sapiens

<220>

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<222> (357) .. (2015)

10

<400> 150

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ggctgccctc ggtccttccc tgccacgttt cgggtcgccc tgcaccccc acccaggctc 180
15 gcttctcttc gaagcgggaa gggcgccttg caggatcctg ccgcccctcc aaccggatcc 240
tgggtctaga gctccccaga gcgaggcgct cgccaggact cctgccccgc caaccctgac 300
cgccgggggg tgccccggg acgtagcgcc gcggagagga agcggcaaag gggacc atg 359

Met

1

20 cgg cgc ctg act cgt cgg ctg gtt ctg cca gtc ttc ggg gtg ctc tgg 407
Arg Arg Leu Thr Arg Arg Leu Val Leu Pro Val Phe Gly Val Leu Trp

5

10

15

atc acg gtg ctg ctg ttc ttc tgg gta acc aag agg aag ttg gag gtg 455
Ile Thr Val Leu Leu Phe Phe Trp Val Thr Lys Arg Lys Leu Glu Val

25

20

25

30

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ccg acg gga cct gaa gtg cag acc cct aag cct tcg gac gct gac tgg 503
 Pro Thr Gly Pro Glu Val Gln Thr Pro Lys Pro Ser Asp Ala Asp Trp
 35 40 45
 gac gac ctg tgg gac cag ttt gat gag cgg cgg tat ctg aat gcc aaa 551
 5 Asp Asp Leu Trp Asp Gln Phe Asp Glu Arg Arg Tyr Leu Asn Ala Lys
 50 55 60 65
 aag tgg cgc gtt ggt gac gac ccc tat aag ctg tat gct ttc aac cag 599
 Lys Trp Arg Val Gly Asp Asp Pro Tyr Lys Leu Tyr Ala Phe Asn Gln
 70 75 80
 10 cgg gag agt gag cgg atc tcc agc aat cgg gcc atc ccg gac act cgc 647
 Arg Glu Ser Glu Arg Ile Ser Ser Asn Arg Ala Ile Pro Asp Thr Arg
 85 90 95
 cat ctg aga tgc aca ctg ctg gtg tat tgc acg gac ctt cca ccc act 695
 His Leu Arg Cys Thr Leu Leu Val Tyr Cys Thr Asp Leu Pro Pro Thr
 15 100 105 110
 agc atc atc atc acc ttc cac aac gag gcc cgc tcc acg ctg ctc agg 743
 Ser Ile Ile Ile Thr Phe His Asn Glu Ala Arg Ser Thr Leu Leu Arg
 115 120 125
 acc atc cgc agt gta tta aac cgc acc cct acg cat ctg atc cgg gaa 791
 20 Thr Ile Arg Ser Val Leu Asn Arg Thr Pro Thr His Leu Ile Arg Glu
 130 135 140 145
 atc ata tta gtg gat gac ttc agc aat gac cct gat gac tgt aaa cag 839
 Ile Ile Leu Val Asp Asp Phe Ser Asn Asp Pro Asp Asp Cys Lys Gln
 150 155 160
 25 ctc atc aag ttg ccc aag gtg aaa tgc ttg cgc aat aat gaa cgg caa 887

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Leu Ile Lys Leu Pro Lys Val Lys Cys Leu Arg Asn Asn Glu Arg Gln
 165 170 175
 ggt ctg gtc cgg tcc cgg att cgg ggc gct gac atc gcc cag ggc acc 935
 Gly Leu Val Arg Ser Arg Ile Arg Gly Ala Asp Ile Ala Gln Gly Thr
 5 180 185 190
 act ctg act ttc ctc gac agc cac tgt gag gtg aac agg gac tgg ctc 983
 Thr Leu Thr Phe Leu Asp Ser His Cys Glu Val Asn Arg Asp Trp Leu
 195 200 205
 cag cct ctg ttg cac agg gtc aaa gag gac tac acg cgg gtg gtg tgc 1031
 10 Gln Pro Leu Leu His Arg Val Lys Glu Asp Tyr Thr Arg Val Val Cys
 210 215 220 225
 cct gtg atc gat atc att aac ctg gac acc ttc acc tac atc gag tct 1079
 Pro Val Ile Asp Ile Ile Asn Leu Asp Thr Phe Thr Tyr Ile Glu Ser
 230 235 240
 15 gcc tcg gag ctc aga ggg ggg ttt gac tgg agc ctc cac ttc cag tgg 1127
 Ala Ser Glu Leu Arg Gly Gly Phe Asp Trp Ser Leu His Phe Gln Trp
 245 250 255
 gag cag ctc tcc cca gag cag aag gct cgg cgc ctg gac ccc acg gag 1175
 Glu Gln Leu Ser Pro Glu Gln Lys Ala Arg Arg Leu Asp Pro Thr Glu
 20 260 265 270
 ccc atc agg act cct atc ata gct gga ggg ctc ttc gtg atc gac aaa 1223
 Pro Ile Arg Thr Pro Ile Ile Ala Gly Gly Leu Phe Val Ile Asp Lys
 275 280 285
 gct tgg ttt gat tac ctg ggg aaa tat gat atg gac atg gac atc tgg 1271
 25 Ala Trp Phe Asp Tyr Leu Gly Lys Tyr Asp Met Asp Met Asp Ile Trp

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	290	295	300	305	
	ggg ggg gag aac ttt gaa atc tcc ttc cga gtg tgg atg tgc ggg ggc				1319
	Gly Gly Glu Asn Phe Glu Ile Ser Phe Arg Val Trp Met Cys Gly Gly				
	310	315	320		
5	agc cta gag atc gtc ccc tgc agc cga gtg ggg cac gtc ttc cgg aag				1367
	Ser Leu Glu Ile Val Pro Cys Ser Arg Val Gly His Val Phe Arg Lys				
	325	330	335		
	aag cac ccc tac gtt ttc cct gat gga aat gcc aac acg tat ata aag				1415
	Lys His Pro Tyr Val Phe Pro Asp Gly Asn Ala Asn Thr Tyr Ile Lys				
10	340	345	350		
	aac acc aag cgg aca gct gaa gtg tgg atg gat gaa tac aag caa tac				1463
	Asn Thr Lys Arg Thr Ala Glu Val Trp Met Asp Glu Tyr Lys Gln Tyr				
	355	360	365		
	tat tac gct gcc cgg cca ttc gcc ctg gag agg ccc ttc ggg aat gtt				1511
15	Tyr Tyr Ala Ala Arg Pro Phe Ala Leu Glu Arg Pro Phe Gly Asn Val				
	370	375	380	385	
	gag agc aga ttg gac ctg agg aag aat ctg cgc tgc cag agc ttc aag				1559
	Glu Ser Arg Leu Asp Leu Arg Lys Asn Leu Arg Cys Gln Ser Phe Lys				
	390	395	400		
20	tgg tac ctg gag aat atc tac cct gaa ctc agc atc ccc aag gag tcc				1607
	Trp Tyr Leu Glu Asn Ile Tyr Pro Glu Leu Ser Ile Pro Lys Glu Ser				
	405	410	415		
	tcc atc cag aag ggc aat atc cga cag aga cag aag tgc ctg gaa tct				1655
	Ser Ile Gln Lys Gly Asn Ile Arg Gln Arg Gln Lys Cys Leu Glu Ser				
25	420	425	430		

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 Gln Arg Gln Asn Asn Gln Glu Thr Pro Asn Leu Lys Leu Ser Pro Cys
 435 440 445
 gcc aag gtc aaa ggc gaa gat gca aag tcc cag gta tgg gcc ttc aca 1751
 5 Ala Lys Val Lys Gly Glu Asp Ala Lys Ser Gln Val Trp Ala Phe Thr
 450 455 460 465
 tac acc cag cag atc ctc cag gag gag ctg tgc ctg tca gtc atc acc 1799
 Tyr Thr Gln Gln Ile Leu Gln Glu Glu Leu Cys Leu Ser Val Ile Thr
 470 475 480
 10 ttg ttc cct ggc gcc cca gtg gtt ctt gtc ctt tgc aag aat gga gat 1847
 Leu Phe Pro Gly Ala Pro Val Val Leu Val Leu Cys Lys Asn Gly Asp
 485 490 495
 gac cga cag caa tgg acc aaa act ggt tcc cac atc gag cac ata gca 1895
 Asp Arg Gln Gln Trp Thr Lys Thr Gly Ser His Ile Glu His Ile Ala
 15 500 505 510
 tcc cac ctc tgc ctc gat aca gat atg ttc ggt gat ggc acc gag aac 1943
 Ser His Leu Cys Leu Asp Thr Asp Met Phe Gly Asp Gly Thr Glu Asn
 515 520 525
 ggc aag gaa atc gtc gtc aac cca tgt gag tcc tca ctc atg agc cag 1991
 20 Gly Lys Glu Ile Val Val Asn Pro Cys Glu Ser Ser Leu Met Ser Gln
 530 535 540 545
 cac tgg gac atg gtg agc tct tga ggaccctgc cagaagcagc aagggccatg 2045
 His Trp Asp Met Val Ser Ser
 550
 25 gggtggtgct tccctggacc agaacagact ggaaactggg cagcaagcag cctgcaacca 2105

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cctcagacat cctggactgg gaggtggagg cagagcccc caggacagga gcaactgtct 2165
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